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OM protein - protein search, using sw model

Run on: May 17, 2005, 10:15:05 ; Search time 23 Seconds

(Without alignments)
759,473 Million cell updates/sec

Title: US-10-063-518-14

Perfect score: 1195

Sequence: 1 MNHLPEMDMVALTGSSQSHL.....EAGSEAEKQDEKPLLEL 234

Scoring table: BLOSUM62

Gapop 10.0 , Gapept 0.5

Searched: 513545 seqs, 7469064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Lifting first 1500 summaries

Database: Issued Patents AA:*

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6: /cgn2_6/ptodata/1/1aa/backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	664	55.6	445	2	US-08-691-814B-6
2	85.5	7.2	449	4	US-09-949-016-8594
3	82.5	6.9	341	2	US-08-846-762-92
4	80.5	6.7	350	4	US-09-489-039A-9711
5	79.5	6.7	406	4	US-09-171-639-6
6	79.5	6.7	406	5	PCT-US94-02107-2
7	79.5	6.7	723	4	US-09-976-594-503
8	78.5	6.6	221	4	US-09-270-767-11033
9	78.5	6.6	221	4	US-09-270-767-56249
10	78.5	6.6	766	4	US-09-724-653-2
11	78.5	6.6	766	4	US-09-724-653-14
12	78.5	6.6	766	4	US-09-724-653-15
13	78.5	6.5	226	4	US-09-248-796A-20444
14	78.5	6.5	251	4	US-09-270-767-43373
15	78.5	6.5	355	4	US-08-833-752-9
16	78.5	6.5	355	4	US-09-938-719-9
17	78.5	6.5	355	4	US-09-939-226B-9
18	78.5	6.4	353	2	US-08-466-103A-14
19	77.7	6.4	353	3	US-09-280-420-2
20	77.7	6.4	353	3	US-09-479-195-2
21	76.5	6.4	435	4	US-09-489-039A-12344
22	76.5	6.4	494	1	US-08-464-340A-4
23	76.5	6.4	494	5	PCT-US94-08449A-4
24	76.5	6.4	195	4	US-09-134-000C-5992
25	75.5	6.4	593	4	US-09-720-317A-22
26	75.5	6.3	263	4	US-09-583-110-3148
27	75.5	6.3	264	4	US-09-107-433-4877

28	75.5	6.3	352	4	US-09-492-709A-293	Sequence 293, App
29	75.5	6.3	355	4	US-09-248-796A-14258	Sequence 14258, A
30	75.5	6.3	397	4	US-09-721-870-105	Sequence 105, App
31	75.5	6.3	433	4	US-09-721-870-107	Sequence 107, App
32	75.5	6.3	471	2	US-08-477-451-20	Sequence 20, App
33	75.5	6.3	499	4	US-09-721-870-40	Sequence 40, App
34	75.5	6.3	467	4	US-09-328-352-5465	Sequence 5465, Ap
35	75.5	6.3	549	4	US-09-134-000C-4375	Sequence 4375, Ap
36	74.5	6.2	355	1	US-08-153-848-28	Sequence 28, App
37	74.5	6.2	355	1	US-08-153-848-32	Sequence 32, App
38	74.5	6.2	355	3	US-09-299-843A-28	Sequence 28, App
39	74.5	6.2	355	3	US-09-299-843A-32	Sequence 32, App
40	74.5	6.2	355	3	US-09-088-337B-28	Sequence 28, App
41	74.5	6.2	355	3	US-09-088-337B-32	Sequence 32, App
42	74.5	6.2	355	4	US-09-170-496D-130	Sequence 130, App
43	74.5	6.2	355	4	US-09-170-496D-232	Sequence 232, App
44	74.5	6.2	355	4	US-09-917-254-68	Sequence 68, App
45	74.5	6.2	355	5	PCT-US93-11153-28	Sequence 28, App
46	74.5	6.2	355	5	PCT-US93-11153-32	Sequence 32, App
47	74.5	6.2	471	1	US-07-996-772A-11	Sequence 11, App
48	74.5	6.2	471	3	US-09-032-742-2	Sequence 2, App
49	74.5	6.2	471	3	US-09-032-742-11	Sequence 11, App
50	74.5	6.2	471	3	US-09-032-742-14	Sequence 14, App
51	74.5	6.2	471	3	US-09-032-742-17	Sequence 17, App
52	74.5	6.2	471	3	US-09-145-864-4	Sequence 4, App
53	74.5	6.2	940	4	US-09-328-352-8165	Sequence 8165, Ap
54	74.5	6.2	154	4	US-09-543-681A-7579	Sequence 7579, Ap
55	74.5	6.2	332	4	US-09-107-433-2662	Sequence 2662, Ap
56	74.5	6.2	332	2	US-08-466-103A-12	Sequence 12, App
57	74.5	6.2	333	2	US-08-896-365-6	Sequence 6, App
58	74.5	6.2	680	4	US-09-248-796A-15089	Sequence 15089, A
59	73.5	6.2	312	4	US-09-543-681A-6267	Sequence 6267, Ap
60	73.5	6.2	400	4	US-09-902-540-11488	Sequence 11488, A
61	73.5	6.2	3033	1	US-07-925-695-9	Sequence 9, App
62	73.5	6.1	199	4	US-09-107-532A-6773	Sequence 6773, Ap
63	73.5	6.1	222	4	US-09-903-456-75	Sequence 75, App
64	73.5	6.1	364	3	US-09-077-675A-16	Sequence 16, App
65	73.5	6.1	364	4	US-09-077-675A-16	Sequence 16, App
66	73.5	6.1	364	4	US-09-762-651A-6	Sequence 6, App
67	73.5	6.1	364	4	US-09-743-875-3	Sequence 3, App
68	73.5	6.1	377	3	US-09-743-875-5	Sequence 5, App
69	73.5	6.1	494	4	US-08-936-165A-533	Sequence 533, App
70	73.5	6.1	494	4	US-09-949-016-7475	Sequence 7475, Ap
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72	73.5	6.1	746	2	US-08-785-431-4	Sequence 4, App
73	73.5	6.1	746	3	US-09-205-048-4	Sequence 4, App
74	73.5	6.1	788	3	US-08-785-431-2	Sequence 2, App
75	73.5	6.1	312	4	US-09-205-048-2	Sequence 2, App
76	72.5	6.1	353	4	US-09-248-796A-20385	Sequence 20385, A
77	72.5	6.1	353	4	US-09-134-000C-5562	Sequence 5562, Ap
78	72.5	6.1	359	4	US-09-134-000C-5442	Sequence 5442, Ap
79	72.5	6.1	448	2	US-08-811-897A-16	Sequence 16, App
80	72.5	6.1	448	2	US-08-855-213-16	Sequence 16, App
81	72.5	6.1	448	3	US-09-201-474-16	Sequence 16, App
82	72.5	6.1	476	2	US-08-811-897A-14	Sequence 14, App
83	72.5	6.1	476	2	US-08-855-213-14	Sequence 14, App
84	72.5	6.1	476	3	US-09-201-474-14	Sequence 14, App
85	72.5	6.1	445	2	US-08-811-897A-17	Sequence 17, App
86	72.5	6.1	445	2	US-08-855-213-17	Sequence 17, App
87	72.5	6.1	445	3	US-09-201-474-17	Sequence 17, App
88	72.5	6.1	513	2	US-08-811-897A-15	Sequence 15, App
89	72.5	6.1	513	2	US-08-855-213-15	Sequence 15, App
90	72.5	6.1	513	3	US-09-201-474-15	Sequence 15, App
91	72.5	6.1	673	4	US-09-949-016-7656	Sequence 7656, Ap
92	72.5	6.0	666	4	US-09-949-016-6546	Sequence 6546, Ap
93	72.5	6.0	741	4	US-09-585-858-11	Sequence 11, App
94	72.5	6.0	741	4	US-10-270-878-11	Sequence 11, App
95	72.5	6.0	1031	4	US-09-538-092-487	Sequence 487, App
96	72.5	6.0	2307	3	US-09-263-833-9	Sequence 2, App
97	72.5	6.0	2307	3	US-09-263-833-9	Sequence 9, App
98	72.5	6.0	2307	3	US-09-263-833-16	Sequence 16, App
99	72.5	6.0	2307	4	US-09-919-901-2	Sequence 2, App
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101	72	6.0	2307	4	US-09-919-901-16	Sequence 16, Appl	174	70	5.9	333	4	US-09-170-496D-16	Sequence 16, Appl
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103	72	6.0	2307	4	US-10-191-966-9	Sequence 9, Appl	176	70	5.9	333	4	US-09-248-796A-17918	Sequence 17918, A
104	72	6.0	2307	4	US-10-191-966-16	Sequence 16, Appl	177	70	5.9	361	4	US-09-270-767-40072	Sequence 40072, A
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108	71.5	6.0	366	2	US-08-896-365-7	Sequence 7, Appl	181	70	5.9	425	4	US-09-107-532A-6574	Sequence 6574, Ap
109	71.5	6.0	382	4	US-09-262-477-2	Sequence 2, Appl	182	70	5.9	470	4	US-09-328-352-15397	Sequence 15397, Ap
110	71.5	6.0	510	4	US-09-679-686B-19	Sequence 19, Appl	183	70	5.9	471	3	US-09-328-114-17	Sequence 17, Appl
111	71.5	6.0	670	4	US-09-575-081B-26	Sequence 26, Appl	184	70	5.9	757	4	US-09-540-236-2346	Sequence 2346, Ap
112	71.5	6.0	724	4	US-09-949-016-10086	Sequence 10086, A	185	69.5	5.8	188	4	US-09-328-352-4951	Sequence 4951, Ap
113	71	5.9	312	1	US-08-118-270-58	Sequence 38, Appl	186	69.5	5.8	270	4	US-09-252-991A-29192	Sequence 29192, A
114	71	5.9	312	5	PCT-US93-08528-38	Sequence 38, Appl	187	69.5	5.8	331	4	US-09-198-452A-778	Sequence 778, App
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116	71	5.9	470	3	US-09-292-071-25	Sequence 25, Appl	189	69.5	5.8	382	4	US-09-169-205D-21	Sequence 21, Appl
117	71	5.9	470	3	US-09-292-071-25	Sequence 25, Appl	190	69.5	5.8	453	4	US-09-583-110-3842	Sequence 3842, Ap
118	71	5.9	470	3	US-09-292-069A-25	Sequence 25, Appl	191	69.5	5.8	461	4	US-09-107-433-3722	Sequence 3722, Ap
119	71	5.9	470	4	US-09-767-013-65	Sequence 25, Appl	192	69.5	5.8	454	4	US-09-489-039A-8154	Sequence 8154, Ap
120	71	5.9	471	4	US-09-292-072-25	Sequence 8, Appl	193	69.5	5.8	557	4	US-10-327-189-4	Sequence 4, Appl
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122	71	5.9	471	1	US-08-117-006-8	Sequence 8, Appl	195	69.5	5.8	557	4	US-09-798-743-1	Sequence 1, Appl
123	71	5.9	471	1	US-08-216-59A-8	Sequence 8, Appl	196	69.5	5.8	557	4	US-09-949-016-6309	Sequence 6309, Ap
124	71	5.9	471	1	US-08-342-358-7	Sequence 7, Appl	197	69.5	5.8	558	4	US-09-438-185A-732	Sequence 732, App
125	71	5.9	471	2	US-08-244-434-2	Sequence 2, Appl	198	69.5	5.8	559	4	US-09-328-352-5924	Sequence 5924, App
126	71	5.9	471	3	US-09-018-351-7	Sequence 7, Appl	199	69.5	5.8	559	4	US-09-489-039A-9425	Sequence 9425, Ap
127	71	5.9	471	3	US-09-032-742-8	Sequence 8, Appl	200	69.5	5.8	599	1	US-08-301-722A-5	Sequence 5, Appl
128	71	5.9	471	3	US-09-145-864-2	Sequence 2, Appl	201	69.5	5.8	610	4	US-09-949-016-7929	Sequence 7929, Ap
129	71	5.9	471	4	US-09-170-496D-122	Sequence 122, App	202	69.5	5.8	660	3	US-09-134-001C-5039	Sequence 5039, Ap
130	71	5.9	471	4	US-09-170-496D-228	Sequence 228, App	203	69.5	5.8	663	3	US-08-959-004-5	Sequence 5, Appl
131	71	5.9	471	5	US-10-092-138A-28	Sequence 28, Appl	204	69.5	5.8	676	4	US-09-949-016-9494	Sequence 9494, Ap
132	71	5.9	471	5	PCT-US93-00149-8	Sequence 8, Appl	205	69.5	5.8	877	4	US-09-165-396-6	Sequence 5, Appl
133	71	5.9	2296	2	US-08-286-819A-27	Sequence 27, Appl	206	69.5	5.8	1028	4	US-09-328-352-5749	Sequence 5749, Ap
134	71	5.9	2296	3	US-08-980-357-87	Sequence 27, Appl	207	69.5	5.8	1684	3	US-08-665-259-25	Sequence 25, Appl
135	70.5	5.9	228	3	US-09-291-922-16	Sequence 16, Appl	208	69.5	5.8	1684	3	US-08-762-500-75	Sequence 75, Appl
136	70.5	5.9	297	4	US-09-328-352-7074	Sequence 7074, Ap	209	69.5	5.8	1704	4	US-09-032-438C-110	Sequence 120, App
137	70.5	5.9	365	3	US-08-155-005A-8	Sequence 8, Appl	210	69.5	5.8	1766	4	US-09-949-016-10796	Sequence 10796, A
138	70.5	5.9	365	3	US-09-363-783-8	Sequence 8, Appl	211	69.5	5.8	193	3	US-08-858-207A-430	Sequence 430, App
139	70.5	5.9	365	4	US-09-661-758A-8	Sequence 8, Appl	212	69	5.8	340	4	US-09-248-796A-15237	Sequence 15237, A
140	70.5	5.9	367	4	US-09-543-681A-4643	Sequence 4643, Ap	213	69	5.8	370	3	US-08-513-974B-26	Sequence 26, Appl
141	70.5	5.9	379	1	US-08-118-270-32	Sequence 32, Appl	214	69	5.8	370	3	US-08-513-974B-333	Sequence 323, App
142	70.5	5.9	379	5	PCT-US93-08528-32	Sequence 32, Appl	215	69	5.8	370	3	US-09-172-353-5	Sequence 5, Appl
143	70.5	5.9	388	3	US-08-155-005A-6	Sequence 6, Appl	216	69	5.8	370	3	US-08-776-971-21	Sequence 21, Appl
144	70.5	5.9	388	3	US-09-363-783-6	Sequence 6, Appl	217	69	5.8	370	3	US-08-776-971-104	Sequence 104, App
145	70.5	5.9	388	4	US-09-661-758A-6	Sequence 6, Appl	218	69	5.8	370	4	US-09-779-955-5	Sequence 5, Appl
146	70.5	5.9	390	3	US-08-155-005A-4	Sequence 4, Appl	219	69	5.8	370	4	US-09-461-436B-26	Sequence 26, Appl
147	70.5	5.9	390	3	US-08-155-005A-17	Sequence 17, Appl	220	69	5.8	370	4	US-09-576-290-21	Sequence 21, Appl
148	70.5	5.9	390	3	US-09-363-783-4	Sequence 4, Appl	221	69	5.8	370	4	US-09-576-290-104	Sequence 104, App
149	70.5	5.9	390	3	US-09-363-783-17	Sequence 17, Appl	222	69	5.8	388	4	US-09-492-709A-378	Sequence 378, App
150	70.5	5.9	390	4	US-09-661-758A-4	Sequence 4, Appl	223	69	5.8	422	4	US-09-489-039A-8418	Sequence 8418, App
151	70.5	5.9	390	4	US-09-661-758A-17	Sequence 17, Appl	224	69	5.8	422	4	US-09-270-767-45540	Sequence 45540, A
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153	70.5	5.9	539	3	US-09-291-922-86	Sequence 26, Appl	226	69	5.8	661	4	US-09-248-796A-20857	Sequence 20857, A
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155	70.5	5.9	539	1	US-08-295-814E-11	Sequence 11, Appl	228	69	5.8	725	4	US-09-489-039A-9425	Sequence 9425, Ap
156	70.5	5.9	539	1	US-08-240-783B-4	Sequence 4, Appl	229	68.5	5.7	129	4	US-09-270-767-36588	Sequence 36588, A
157	70.5	5.9	539	3	US-08-753-985-10	Sequence 10, Appl	230	68.5	5.7	139	4	US-09-170-767-51805	Sequence 51805, A
158	70.5	5.9	539	3	US-09-084-813-4	Sequence 4, Appl	231	68.5	5.7	178	4	US-09-134-000C-37174	Sequence 37174, Ap
159	70.5	5.9	539	5	US-09-343-361-11	Sequence 11, Appl	232	68.5	5.7	199	3	US-08-478-316-36	Sequence 36, Appl
160	70.5	5.9	539	5	PCT-US92-09662-4	Sequence 4, Appl	233	68.5	5.7	199	3	US-09-019-793A-36	Sequence 36, Appl
161	70.5	5.9	1027	2	US-08-551-437-2	Sequence 2, Appl	234	68.5	5.7	200	4	US-09-601-326-36	Sequence 36, Appl
162	70.5	5.9	1027	3	US-09-004-225-2	Sequence 2, Appl	235	68.5	5.7	225	4	US-09-543-681A-7698	Sequence 7698, App
163	70.5	5.9	1027	3	US-09-084-346-2	Sequence 2, Appl	236	68.5	5.7	257	2	US-08-996-365-8	Sequence 8, Appl
164	70.5	5.9	1027	3	US-09-104-704-2	Sequence 2, Appl	237	68.5	5.7	297	4	US-09-448-796A-20728	Sequence 20728, A
165	70.5	5.9	1027	1	US-08-769-309A-5	Sequence 5, Appl	238	68.5	5.7	377	3	US-09-161-994A-12	Sequence 12, Appl
166	70.5	5.9	1780	3	US-08-994-570-5	Sequence 5, Appl	239	68.5	5.7	382	3	US-09-542-733-2	Sequence 2, Appl
167	70.5	5.9	1781	4	US-09-961-403-13	Sequence 13, Appl	240	68.5	5.7	383	1	US-08-196-989B-4	Sequence 4, Appl
168	70	5.9	1482	4	US-09-248-796A-27134	Sequence 27134, A	241	68.5	5.7	383	2	US-08-760-936-4	Sequence 4, Appl
169	70	5.9	153	2	US-08-896-365-9	Sequence 9, Appl	242	68.5	5.7	383	4	US-09-125-024-4	Sequence 4, Appl
170	70	5.9	298	4	US-09-270-767-44605	Sequence 34605, A	243	68.5	5.7	417	4	US-09-134-000C-5002	Sequence 5002, Ap
171	70	5.9	298	4	US-09-767-49822	Sequence 49822, A	244	68.5	5.7	420	2	US-08-466-103A-2	Sequence 2, Appl
172	70	5.9	307	4	US-09-583-110-5003	Sequence 5003, Ap	245	68.5	5.7	437	4	US-09-328-352-5102	Sequence 5102, Ap
173	70	5.9	333	1	US-08-148-215A-4	Sequence 4, Appl	246	68.5	5.7	444	3	US-08-482-746-15	Sequence 15, Appl

247	68.5	5.7	444	4	US-09-580-734-15	Sequence 15, Appl	320	68	5.7	472	4	US-09-951-217-36	Sequence 36, Appl
248	68.5	5.7	444	4	US-08-374-009-15	Sequence 15, Appl	321	68	5.7	480	1	US-08-440-103-22	Sequence 22, Appl
249	68.5	5.7	444	4	US-09-131-724-15	Sequence 15, Appl	322	68	5.7	480	1	US-08-440-542-22	Sequence 22, Appl
250	68.5	5.7	444	4	US-09-631-603-11	Sequence 11, Appl	323	68	5.7	480	1	US-08-231-568-22	Sequence 22, Appl
251	68.5	5.7	448	2	US-08-811-897A-22	Sequence 22, Appl	324	68	5.7	480	1	US-08-440-210-22	Sequence 22, Appl
252	68.5	5.7	448	2	US-08-855-213-22	Sequence 22, Appl	325	68	5.7	480	3	US-09-046-604-22	Sequence 22, Appl
253	68.5	5.7	448	3	US-09-201-474-22	Sequence 22, Appl	326	68	5.7	488	1	US-08-115-365-2	Sequence 2, Appl
254	68.5	5.7	468	4	US-09-631-603-19	Sequence 19, Appl	327	68	5.7	488	1	US-08-586-897-2	Sequence 2, Appl
255	68.5	5.7	468	4	US-09-826-509-553	Sequence 553, App	328	68	5.7	488	4	US-09-826-509-561	Sequence 561, App
256	68.5	5.7	475	2	US-08-811-897A-26	Sequence 26, Appl	329	68	5.7	503	1	US-08-484-840-4	Sequence 4, Appl
257	68.5	5.7	475	2	US-08-855-213-26	Sequence 26, Appl	330	68	5.7	503	1	US-08-483-094-4	Sequence 4, Appl
258	68.5	5.7	475	3	US-09-201-474-26	Sequence 26, Appl	331	68	5.7	727	5	US-08-424-424B-2	Sequence 2, Appl
259	68.5	5.7	476	2	US-08-811-897A-24	Sequence 24, Appl	332	68	5.7	727	5	PCT-US94-05362A-2	Sequence 2, Appl
260	68.5	5.7	476	2	US-08-811-897A-28	Sequence 28, Appl	333	68	5.7	859	4	US-09-538-092-206	Sequence 206, App
261	68.5	5.7	476	2	US-08-855-213-24	Sequence 24, Appl	334	68	5.7	908	3	US-08-823-110-1	Sequence 1, Appl
262	68.5	5.7	476	2	US-08-855-213-28	Sequence 28, Appl	335	68	5.7	908	3	US-08-604-298-1	Sequence 1, Appl
263	68.5	5.7	476	3	US-09-201-474-24	Sequence 24, Appl	336	68	5.7	968	3	US-08-551-999A-7	Sequence 7, Appl
264	68.5	5.7	476	3	US-09-201-474-28	Sequence 28, Appl	337	68	5.7	968	3	US-09-385-752-7	Sequence 7, Appl
265	68.5	5.7	525	2	US-08-811-897A-23	Sequence 23, Appl	338	68	5.7	968	4	US-09-949-016-5914	Sequence 5914, Ap
266	68.5	5.7	525	2	US-08-855-213-23	Sequence 23, Appl	339	68	5.7	987	4	US-09-949-016-10368	Sequence 10368, A
267	68.5	5.7	525	3	US-09-201-474-23	Sequence 23, Appl	340	68	5.7	2013	1	US-08-324-977-12	Sequence 12, Appl
268	68.5	5.7	538	4	US-09-139-476-469	Sequence 469, App	341	68	5.7	2013	2	US-08-384-616-12	Sequence 12, Appl
269	68.5	5.7	552	2	US-08-811-897A-27	Sequence 27, Appl	342	68	5.7	2013	2	US-08-304-686A-12	Sequence 12, Appl
270	68.5	5.7	552	2	US-08-855-213-27	Sequence 27, Appl	343	68	5.7	2013	3	US-09-315-850-12	Sequence 12, Appl
271	68.5	5.7	552	2	US-09-201-474-27	Sequence 27, Appl	344	68	5.7	2620	1	US-08-324-977-32	Sequence 32, Appl
272	68.5	5.7	553	2	US-08-811-897A-25	Sequence 25, Appl	345	68	5.7	2620	2	US-08-384-616-32	Sequence 32, Appl
273	68.5	5.7	553	2	US-08-811-897A-29	Sequence 29, Appl	346	68	5.7	2620	2	US-08-304-686A-32	Sequence 32, Appl
274	68.5	5.7	553	2	US-08-855-213-25	Sequence 25, Appl	347	68	5.7	2620	3	US-09-315-850-32	Sequence 32, Appl
275	68.5	5.7	553	2	US-08-855-213-29	Sequence 29, Appl	348	68	5.7	2621	1	US-08-324-977-36	Sequence 36, Appl
276	68.5	5.7	553	3	US-09-201-474-25	Sequence 25, Appl	349	68	5.7	2621	2	US-08-384-616-36	Sequence 36, Appl
277	68.5	5.7	553	3	US-09-201-474-29	Sequence 29, Appl	350	68	5.7	2621	3	US-08-304-686A-36	Sequence 36, Appl
278	68.5	5.7	570	4	US-09-949-016-8907	Sequence 8907, Ap	351	68	5.7	3010	1	US-09-315-850-36	Sequence 36, Appl
279	68.5	5.7	660	4	US-09-252-991A-29885	Sequence 29885, A	352	68	5.7	3010	1	US-08-324-977-2	Sequence 2, Appl
280	68.5	5.7	762	4	US-09-107-532A-5096	Sequence 5096, Ap	353	68	5.7	3010	1	US-08-384-616-14	Sequence 14, Appl
281	68.5	5.7	762	4	US-09-724-653-7	Sequence 7, Appl	354	68	5.7	3010	2	US-08-384-616-12	Sequence 12, Appl
282	68.5	5.7	1296	4	US-09-462-136-9	Sequence 9, Appl	355	68	5.7	3010	2	US-08-304-686A-12	Sequence 2, Appl
283	68	5.7	188	4	US-09-270-767-36930	Sequence 36930, A	356	68	5.7	3010	2	US-08-304-686A-14	Sequence 14, Appl
284	68	5.7	188	4	US-09-270-767-52147	Sequence 52147, A	357	68	5.7	3010	2	US-09-315-850-2	Sequence 2, Appl
285	68	5.7	247	4	US-09-603-208A-152	Sequence 152, App	358	68	5.7	3010	3	US-09-315-850-14	Sequence 14, Appl
286	68	5.7	247	3	US-09-053-197A-7	Sequence 7, Appl	359	68	5.7	3010	3	US-09-248-796A-20156	Sequence 20156, A
287	68	5.7	258	3	US-09-085-761A-7	Sequence 7, Appl	360	67.5	5.6	210	4	US-09-440-236-3093	Sequence 3093, Ap
288	68	5.7	309	4	US-09-328-352-5344	Sequence 6344, Ap	361	67.5	5.6	253	4	US-09-440-236-3093	Sequence 3093, Ap
289	68	5.7	346	4	US-09-585-876-2	Sequence 2, Appl	362	67.5	5.6	306	4	US-09-252-991A-32161	Sequence 32161, A
290	68	5.7	355	1	US-08-012-988A-2	Sequence 2, Appl	363	67.5	5.6	350	2	US-08-966-316-16	Sequence 16, Appl
291	68	5.7	355	1	US-08-450-393A-5	Sequence 5, Appl	364	67.5	5.6	350	4	US-09-721-908-2	Sequence 2, Appl
292	68	5.7	355	3	US-08-446-669-5	Sequence 5, Appl	365	67.5	5.6	350	4	US-09-721-908-2	Sequence 2, Appl
293	68	5.7	355	4	US-09-239-938-1	Sequence 1, Appl	366	67.5	5.6	350	4	US-09-721-908-2	Sequence 2, Appl
294	68	5.7	355	4	US-09-886-319A-14	Sequence 14, Appl	367	67.5	5.6	457	4	US-09-543-681A-6044	Sequence 6044, Ap
295	68	5.7	355	4	US-10-039-659A-13	Sequence 13, Appl	368	67.5	5.6	459	4	US-09-694-519-3	Sequence 3, Appl
296	68	5.7	355	4	US-09-961-068-1	Sequence 1, Appl	369	67.5	5.6	459	4	US-09-694-519-8	Sequence 8, Appl
297	68	5.7	355	4	US-09-625-573-5	Sequence 5, Appl	370	67.5	5.6	515	4	US-09-869-433-2	Sequence 2, Appl
298	68	5.7	355	4	US-09-960-547-1	Sequence 1, Appl	371	67.5	5.6	515	4	US-09-198-452A-369	Sequence 369, App
299	68	5.7	355	5	PCT-US95-00476-5	Sequence 5, Appl	372	67.5	5.6	544	4	US-09-438-185A-353	Sequence 353, App
300	68	5.7	373	4	US-09-107-532A-7048	Sequence 7048, Ap	373	67.5	5.6	544	4	US-09-252-991A-17104	Sequence 17104, A
301	68	5.7	414	4	US-09-489-039A-10869	Sequence 10869, A	374	67.5	5.6	865	4	US-09-252-991A-18683	Sequence 18683, A
302	68	5.7	426	4	US-09-486-132-2	Sequence 2, Appl	375	67.5	5.6	1234	2	US-08-811-897A-56	Sequence 56, Appl
303	68	5.7	471	3	US-08-492-459-14	Sequence 14, Appl	376	67.5	5.6	1234	3	US-09-201-474-56	Sequence 56, Appl
304	68	5.7	471	3	US-08-423-752-14	Sequence 14, Appl	377	67.5	5.6	1411	4	US-09-338-092-413	Sequence 413, App
305	68	5.7	471	3	US-08-716-873-8	Sequence 8, Appl	378	67.5	5.6	2158	4	US-10-144-198-34	Sequence 34, Appl
306	68	5.7	471	3	US-08-716-873-8	Sequence 8, Appl	379	67.5	5.6	2265	4	US-10-144-198-35	Sequence 35, Appl
307	68	5.7	471	3	US-09-368-431-8	Sequence 8, Appl	380	67.5	5.6	2318	3	US-09-091-219-24	Sequence 24, Appl
308	68	5.7	471	3	US-09-368-431-8	Sequence 8, Appl	381	67.5	5.6	2318	4	US-09-660-541-24	Sequence 24, Appl
309	68	5.7	471	3	US-09-368-431-8	Sequence 8, Appl	382	67.5	5.6	2697	4	US-10-144-198-12	Sequence 12, Appl
310	68	5.7	471	4	US-09-414-006-14	Sequence 14, Appl	383	67	5.6	153	4	US-09-198-452A-329	Sequence 329, App
311	68	5.7	471	4	US-09-414-006-14	Sequence 14, Appl	384	67	5.6	153	4	US-09-438-185A-314	Sequence 314, App
312	68	5.7	471	4	US-09-951-217-8	Sequence 8, Appl	385	67	5.6	159	4	US-09-302-540-13804	Sequence 13804, A
313	68	5.7	471	4	US-09-792-024-68	Sequence 28, Appl	386	67	5.6	164	4	US-08-478-316-32	Sequence 32, Appl
314	68	5.7	472	3	US-08-492-459-22	Sequence 22, Appl	387	67	5.6	199	3	US-09-019-793A-32	Sequence 32, Appl
315	68	5.7	472	3	US-08-423-752-22	Sequence 22, Appl	388	67	5.6	199	3	US-08-131-625B-11	Sequence 11, Appl
316	68	5.7	472	3	US-08-716-873-36	Sequence 36, Appl	389	67	5.6	200	4	US-08-301-435-15	Sequence 15, Appl
317	68	5.7	472	3	US-09-368-431-36	Sequence 36, Appl	390	67	5.6	200	4	US-09-601-326-32	Sequence 32, Appl
318	68	5.7	472	3	US-09-414-006-22	Sequence 22, Appl	391	67	5.6	200	5	PCT-US95-10904-15	Sequence 15, Appl
319	68	5.7	472	4	US-09-447-223-22	Sequence 22, Appl	392	67	5.6	200	5	PCT-US95-10904-15	Sequence 15, Appl

393	67	5.6	207	4	US-08-811-519-26	Sequence 26, App1	466	66.5	5.6	849	4	US-09-949-016-8846	Sequence 8846, Ap
394	67	5.6	272	4	US-09-270-767-37728	Sequence 37728, A	467	66.5	5.6	849	4	US-09-949-016-8847	Sequence 8847, Ap
395	67	5.6	272	4	US-09-270-767-52945	Sequence 52945, A	468	66.5	5.6	853	4	US-09-949-016-8875	Sequence 8875, Ap
396	67	5.6	282	4	US-09-270-767-35735	Sequence 35735, A	469	66.5	5.6	853	4	US-09-949-016-8276	Sequence 8276, Ap
397	67	5.6	282	4	US-09-270-767-50952	Sequence 50952, A	470	66.5	5.6	977	4	US-09-134-000C-55653	Sequence 5563, Ap
398	67	5.6	295	3	US-09-372-422A-38	Sequence 38, App1	471	66.5	5.6	1887	4	US-09-792-024-98	Sequence 98, App1
399	67	5.6	360	4	US-09-107-532A-4523	Sequence 4523, Ap	472	66.5	5.6	2261	4	US-08-444-818-66	Sequence 66, App1
400	67	5.6	464	4	US-09-248-796A-18187	Sequence 18187, A	473	66.5	5.6	2894	2	US-08-466-975A-23	Sequence 23, App1
401	67	5.6	479	4	US-09-543-681A-6605	Sequence 6605, Ap	474	66.5	5.6	2894	2	US-08-391-671A-23	Sequence 23, App1
402	67	5.6	480	1	US-08-440-103-18	Sequence 18, App1	475	66.5	5.6	2894	3	US-08-467-902A-23	Sequence 23, App1
403	67	5.6	480	1	US-08-440-542-18	Sequence 18, App1	476	66.5	5.6	2894	4	US-09-275-265-23	Sequence 23, App1
404	67	5.6	480	1	US-08-231-368-18	Sequence 18, App1	477	66.5	5.6	2894	3	US-09-941-611-23	Sequence 23, App1
405	67	5.6	480	1	US-08-440-210-18	Sequence 18, App1	478	66.5	5.6	2955	2	US-08-443-260-3	Sequence 3, App1
406	67	5.6	480	3	US-09-046-604-18	Sequence 18, App1	479	66.5	5.6	2955	3	US-08-442-805A-3	Sequence 3, App1
407	67	5.6	496	6	US-10-146-704-3	Sequence 3, App1	480	66.5	5.6	2955	3	US-08-443-900A-3	Sequence 3, App1
408	67	5.6	733	4	US-09-489-039A-7885	Sequence 7885, Ap	481	66.5	5.6	2955	3	US-08-444-818-124	Sequence 124, App
409	67	5.6	978	4	US-09-585-858-50	Sequence 20, App1	482	66.5	5.6	2955	3	US-08-249-843-3	Sequence 3, App1
410	67	5.6	978	4	US-10-270-878-20	Sequence 20, App1	483	66.5	5.6	2955	3	US-08-444-818-138	Sequence 138, App
411	67	5.6	1093	4	US-09-248-796A-17108	Sequence 17108, A	484	66.5	5.6	3010	3	US-09-014-416-3	Sequence 3, App1
412	67	5.6	1174	1	US-08-040-751-3	Sequence 3, App1	485	66.5	5.6	3011	1	US-08-440-103-36	Sequence 36, App1
413	67	5.6	1174	1	US-08-291-368-2	Sequence 2, App1	486	66.5	5.6	3011	1	US-08-440-542-36	Sequence 36, App1
414	67	5.6	1174	2	US-08-962-190-2	Sequence 2, App1	487	66.5	5.6	3011	1	US-07-910-760-10	Sequence 10, App1
415	67	5.6	1174	5	PCT-US95-10310-2	Sequence 2, App1	488	66.5	5.6	3011	1	US-08-440-519-10	Sequence 10, App1
416	67	5.6	1174	6	5164180-4	Patent No. 5164180	489	66.5	5.6	3011	1	US-08-231-368-36	Sequence 36, App1
417	67	5.6	1174	6	5164180-4	Patent No. 5164180	490	66.5	5.6	3011	1	US-08-440-210-36	Sequence 36, App1
418	67	5.6	1242	2	US-08-680-326-33	Sequence 33, App1	491	66.5	5.6	3011	2	US-08-833-678A-6	Sequence 6, App1
419	67	5.6	1242	4	US-09-904-065-12	Sequence 12, App1	492	66.5	5.6	3011	2	US-08-444-818-177	Sequence 177, App
420	67	5.6	1242	4	US-09-904-065-13	Sequence 13, App1	493	66.5	5.6	3011	3	US-09-014-416-5	Sequence 5, App1
421	67	5.6	3010	4	US-09-539-601-3	Sequence 3, App1	494	66.5	5.6	3011	3	US-08-529-169A-6	Sequence 6, App1
422	67	5.6	3010	4	US-09-539-601-21	Sequence 21, App1	495	66.5	5.6	3011	3	US-09-388-874-2	Sequence 2, App1
423	67	5.6	3010	4	US-09-539-601-27	Sequence 27, App1	496	66.5	5.6	3011	3	US-09-046-604-36	Sequence 36, App1
424	67	5.6	3010	4	US-09-539-601-53	Sequence 33, App1	497	66.5	5.6	3011	3	US-08-440-549-10	Sequence 10, App1
425	67	5.6	3287	2	US-08-477-451-7	Sequence 7, App1	498	66.5	5.6	3011	3	US-08-850-328-1	Sequence 1, App1
426	67	5.6	197	4	US-09-134-000C-4925	Sequence 4925, Ap	499	66.5	5.6	3011	4	US-09-483-799-6	Sequence 6, App1
427	66.5	5.6	200	3	US-08-686-968C-9	Sequence 9, App1	500	66.5	5.6	3011	4	US-09-916-359-2	Sequence 2, App1
428	66.5	5.6	243	4	US-09-328-352-7321	Sequence 7321, Ap	501	66.5	5.6	3011	5	PCT-US91-02228-10	Sequence 10, App1
429	66.5	5.6	288	2	US-08-466-103A-6	Sequence 6, App1	502	66	5.5	192	4	US-09-270-767-61535	Sequence 61535, A
430	66.5	5.6	289	4	US-09-248-796A-17919	Sequence 17919, A	503	66	5.5	219	4	US-09-248-796A-15621	Sequence 15621, A
431	66.5	5.6	293	4	US-09-248-796A-18278	Sequence 18278, A	504	66	5.5	282	4	US-09-107-532A-5717	Sequence 5717, Ap
432	66.5	5.6	341	4	US-09-248-796A-18985	Sequence 18985, A	505	66	5.5	289	3	US-09-134-001C-2917	Sequence 2917, Ap
433	66.5	5.6	341	4	US-09-291-922-14	Sequence 14, App1	506	66	5.5	302	4	US-09-107-532A-4973	Sequence 4973, Ap
434	66.5	5.6	359	4	US-09-828-523A-14	Sequence 14, App1	507	66	5.5	316	4	US-09-328-352-6592	Sequence 6592, Ap
435	66.5	5.6	370	4	US-09-828-523A-74	Sequence 74, App1	508	66	5.5	318	4	US-09-270-767-45996	Sequence 45996, A
436	66.5	5.6	384	4	US-09-949-016-6494	Sequence 6494, Ap	509	66	5.5	370	3	US-09-172-353-7	Sequence 7, App1
437	66.5	5.6	389	4	US-09-134-000C-3706	Sequence 3706, Ap	510	66	5.5	370	4	US-08-776-971-140	Sequence 140, App
438	66.5	5.6	397	4	US-09-902-540-13316	Sequence 13316, A	511	66	5.5	370	4	US-09-799-955-7	Sequence 7, App1
439	66.5	5.6	413	4	US-09-328-352-5589	Sequence 5589, Ap	512	66	5.5	370	4	US-09-576-290-140	Sequence 140, App
440	66.5	5.6	430	4	US-09-583-110-4230	Sequence 4230, Ap	513	66	5.5	381	2	US-08-845-566-3	Sequence 3, App1
441	66.5	5.6	437	4	US-09-107-433-3678	Sequence 3678, Ap	514	66	5.5	381	2	US-08-467-948A-28	Sequence 28, App1
442	66.5	5.6	454	3	US-08-444-818-73	Sequence 73, App1	515	66	5.5	381	3	US-08-852-824-18	Sequence 18, App1
443	66.5	5.6	468	4	US-09-248-796A-27314	Sequence 27314, A	516	66	5.5	381	3	US-08-467-947A-28	Sequence 28, App1
444	66.5	5.6	480	1	US-08-440-103-14	Sequence 14, App1	517	66	5.5	381	4	US-09-731-030A-17	Sequence 17, App1
445	66.5	5.6	480	1	US-08-440-542-14	Sequence 14, App1	518	66	5.5	381	5	PCT-US96-10618-4	Sequence 4, App1
446	66.5	5.6	480	1	US-08-231-368-14	Sequence 14, App1	519	66	5.5	405	4	US-09-799-978-38	Sequence 38, App1
447	66.5	5.6	480	1	US-08-440-210-14	Sequence 14, App1	520	66	5.5	412	4	US-10-138-701-59	Sequence 59, App1
448	66.5	5.6	480	3	US-09-046-604-14	Sequence 14, App1	521	66	5.5	433	4	US-09-134-000C-6536	Sequence 6536, Ap
449	66.5	5.6	537	4	US-09-489-039A-14149	Sequence 14149, A	522	66	5.5	447	4	US-09-825-923-2	Sequence 2, App1
450	66.5	5.6	550	1	US-08-121-057-4	Sequence 4, App1	523	66	5.5	450	4	US-09-825-923-4	Sequence 4, App1
451	66.5	5.6	550	2	US-08-509-187D-4	Sequence 4, App1	524	66	5.5	582	4	US-09-721-870-179	Sequence 179, App
452	66.5	5.6	550	2	US-09-121-396-4	Sequence 4, App1	525	66	5.5	583	4	US-09-270-767-38131	Sequence 38131, A
453	66.5	5.6	550	5	PCT-US93-09704A-4	Sequence 4, App1	526	66	5.5	583	4	US-09-270-767-53348	Sequence 53348, A
454	66.5	5.6	557	4	US-09-248-796A-15455	Sequence 15455, A	527	66	5.5	1250	4	US-08-938-291A-9	Sequence 9, App1
455	66.5	5.6	627	4	US-09-328-352-4917	Sequence 4917, Ap	528	66	5.5	1250	4	US-09-589-619-9	Sequence 9, App1
456	66.5	5.6	663	3	US-08-824-057-3	Sequence 3, App1	529	65.5	5.5	145	4	US-09-134-000C-3453	Sequence 3453, Ap
457	66.5	5.6	663	3	US-09-415-582-3	Sequence 3, App1	530	65.5	5.5	155	4	US-09-134-000C-3721	Sequence 3721, Ap
458	66.5	5.6	663	3	US-09-693-596-4	Sequence 4, App1	531	65.5	5.5	166	3	US-09-134-001C-4279	Sequence 4279, Ap
459	66.5	5.6	738	3	US-08-867-611-35	Sequence 35, App1	532	65.5	5.5	210	4	US-09-538-092-121	Sequence 121, App
460	66.5	5.6	738	4	US-09-690-359-35	Sequence 35, App1	533	65.5	5.5	291	4	US-09-252-991A-35938	Sequence 32938, A
461	66.5	5.6	738	5	PCT-US92-06965A-5	Sequence 5, App1	534	65.5	5.5	356	4	US-09-107-532A-6286	Sequence 6286, Ap
462	66.5	5.6	750	4	US-09-949-016-7201	Sequence 7201, Ap	535	65.5	5.5	369	3	US-09-172-353-6	Sequence 6, App1
463	66.5	5.6	750	4	US-09-949-016-7202	Sequence 7202, Ap	536	65.5	5.5	369	4	US-09-799-955-6	Sequence 6, App1
464	66.5	5.6	801	4	US-09-710-279-90	Sequence 90, App1	537	65.5	5.5	369	4	US-09-170-496D-26	Sequence 26, App1
465	66.5	5.6	802	3	US-09-134-001C-3741	Sequence 3741, Ap	538	65.5	5.5	369	4	US-09-170-496D-178	Sequence 178, App

539	65.5	5.5	407	4	US-09-252-991A-21511	Sequence 21511, A	612	64.5	5.4	328	4	US-09-489-039A-13216	Sequence 13216, A
540	65.5	5.5	459	4	US-09-694-519-4	Sequence 4, Appl1	613	64.5	5.4	333	4	US-09-107-532A-4886	Sequence 4886, Ap
541	65.5	5.5	468	4	US-09-252-991A-17314	Sequence 17314, A	614	64.5	5.4	344	2	US-08-726-575A-2	Sequence 2, Appl1
542	65.5	5.5	467	4	US-09-583-110-4658	Sequence 4658, Ap	615	64.5	5.4	349	3	US-09-134-001C-4519	Sequence 4519, Ap
543	65.5	5.5	490	4	US-09-107-433-4640	Sequence 4640, Ap	616	64.5	5.4	393	4	US-09-270-767C-42317	Sequence 42317, A
544	65.5	5.5	432	4	US-09-107-532A-6945	Sequence 6945, Ap	617	64.5	5.4	394	4	US-09-107-433-3892	Sequence 3892, Ap
545	65.5	5.5	556	4	US-09-248-796A-15726	Sequence 15726, A	618	64.5	5.4	398	4	US-09-583-110-4666	Sequence 4666, Ap
546	65.5	5.5	630	3	US-09-342-647-2	Sequence 2, Appl1	619	64.5	5.4	400	4	US-09-826-509-491	Sequence 491, App
547	65.5	5.5	718	4	US-09-657-960-3	Sequence 3, Appl1	620	64.5	5.4	407	4	US-09-328-352-5605	Sequence 5605, Ap
548	65.5	5.5	860	1	US-08-032-817-4	Sequence 4, Appl1	621	64.5	5.4	411	2	US-08-336-031-2	Sequence 2, Appl1
549	65.5	5.5	860	3	US-08-485-128-4	Sequence 4, Appl1	622	64.5	5.4	411	2	US-08-902-853-7	Sequence 7, Appl1
550	65.5	5.5	860	4	US-09-804-778A-8	Sequence 8, Appl1	623	64.5	5.4	411	5	PCT-US95-06725-2	Sequence 32, Appl1
551	65.5	5.5	860	4	US-09-824-637-4	Sequence 4, Appl1	624	64.5	5.4	413	4	US-09-799-978-32	Sequence 72, Appl1
552	65.5	5.5	959	4	US-09-248-796A-20776	Sequence 20776, A	625	64.5	5.4	418	5	PCT-US94-03321-72	Sequence 2, Appl1
553	65.5	5.5	1226	2	US-08-540-804-12	Sequence 12, Appl1	626	64.5	5.4	437	3	US-09-353-332-2	Sequence 2, Appl1
554	65.5	5.5	1226	2	US-08-218-265-12	Sequence 12, Appl1	627	64.5	5.4	437	1	US-07-781-254A-2	Sequence 2, Appl1
555	65.5	5.5	1226	3	US-08-521-872-12	Sequence 12, Appl1	628	64.5	5.4	446	1	US-07-781-254A-3	Sequence 3, Appl1
556	65.5	5.5	1236	3	US-08-590-399-12	Sequence 12, Appl1	629	64.5	5.4	447	4	US-09-352-991A-20563	Sequence 20563, A
557	65.5	5.5	1410	2	US-08-470-058-4	Sequence 4, Appl1	630	64.5	5.4	448	2	US-08-811-897A-18	Sequence 18, Appl1
558	65.5	5.5	1410	3	US-09-037-188-4	Sequence 4, Appl1	631	64.5	5.4	448	2	US-08-855-213-18	Sequence 18, Appl1
559	65.5	5.5	1410	3	US-09-285-310-4	Sequence 4, Appl1	632	64.5	5.4	448	3	US-09-201-474-18	Sequence 18, Appl1
560	65	5.4	126	4	US-09-107-532A-3813	Sequence 3813, Ap	633	64.5	5.4	444	4	US-09-107-532A-5509	Sequence 5509, Ap
561	65	5.4	181	3	US-09-126-640-10	Sequence 10, Appl1	634	64.5	5.4	467	2	US-08-811-897A-19	Sequence 19, Appl1
562	65	5.4	181	3	US-09-288-292A-10	Sequence 10, Appl1	635	64.5	5.4	467	2	US-08-855-213-19	Sequence 19, Appl1
563	65	5.4	182	3	US-08-826-246-8	Sequence 8, Appl1	636	64.5	5.4	467	3	US-09-201-474-19	Sequence 19, Appl1
564	65	5.4	182	3	US-08-944-495-8	Sequence 8, Appl1	637	64.5	5.4	476	2	US-08-855-213-20	Sequence 20, Appl1
565	65	5.4	182	3	US-08-925-588-8	Sequence 8, Appl1	638	64.5	5.4	476	2	US-08-855-213-20	Sequence 20, Appl1
566	65	5.4	182	4	US-09-372-044-8	Sequence 8, Appl1	639	64.5	5.4	476	2	US-09-201-474-20	Sequence 20, Appl1
567	65	5.4	182	4	US-08-825-486-8	Sequence 8, Appl1	640	64.5	5.4	482	4	US-09-107-532A-4512	Sequence 4512, Ap
568	65	5.4	182	4	US-08-826-248-8	Sequence 8, Appl1	641	64.5	5.4	483	4	US-09-134-000C-4234	Sequence 4234, Ap
569	65	5.4	193	4	US-09-328-352-6034	Sequence 6034, Ap	642	64.5	5.4	486	3	US-09-291-922-10	Sequence 10, Appl1
570	65	5.4	223	4	US-10-162-012-9	Sequence 9, Appl1	643	64.5	5.4	487	4	US-09-349-016-9649	Sequence 9649, Ap
571	65	5.4	222	4	US-09-903-456-79	Sequence 79, Appl1	644	64.5	5.4	484	2	US-09-031-392-5	Sequence 5, Appl1
572	65	5.4	228	4	US-09-949-016-8160	Sequence 8160, Ap	645	64.5	5.4	494	4	US-09-299-549-5	Sequence 5, Appl1
573	65	5.4	282	4	US-09-107-532A-5538	Sequence 5538, Ap	646	64.5	5.4	494	3	US-09-610-417-5	Sequence 5, Appl1
574	65	5.4	311	4	US-09-252-991A-19489	Sequence 19489, A	647	64.5	5.4	495	2	US-08-811-897A-21	Sequence 21, Appl1
575	65	5.4	322	4	US-09-538-092-506	Sequence 506, App	648	64.5	5.4	495	2	US-08-855-213-21	Sequence 21, Appl1
576	65	5.4	326	3	US-09-095-163-2	Sequence 2, Appl1	649	64.5	5.4	495	3	US-09-201-474-21	Sequence 21, Appl1
577	65	5.4	326	3	US-09-485-648-6	Sequence 6, Appl1	650	64.5	5.4	497	4	US-09-521-1958-27	Sequence 27, Appl1
578	65	5.4	322	4	US-09-503-565-6	Sequence 6, Appl1	651	64.5	5.4	557	4	US-09-798-743-3	Sequence 3, Appl1
579	65	5.4	322	4	US-09-485-649-6	Sequence 6, Appl1	652	64.5	5.4	576	3	US-09-448-767A-16	Sequence 16, Appl1
580	65	5.4	375	4	US-09-799-978-6	Sequence 6, Appl1	653	64.5	5.4	576	4	US-08-948-564-16	Sequence 16, Appl1
581	65	5.4	401	4	US-09-799-978-8	Sequence 8, Appl1	654	64.5	5.4	747	3	US-09-291-922-2	Sequence 2, Appl1
582	65	5.4	415	1	US-08-110-386A-2	Sequence 2, Appl1	655	64.5	5.4	757	4	US-09-585-858-24	Sequence 24, Appl1
583	65	5.4	415	3	US-08-482-746-2	Sequence 2, Appl1	656	64.5	5.4	757	4	US-10-270-878A-24	Sequence 24, Appl1
584	65	5.4	415	4	US-09-580-734-2	Sequence 2, Appl1	657	64.5	5.4	757	4	US-09-585-858-24	Sequence 24, Appl1
585	65	5.4	415	4	US-08-374-009-2	Sequence 2, Appl1	658	64.5	5.4	2146	4	US-09-949-016-6947	Sequence 6947, Ap
586	65	5.4	415	4	US-09-191-724-2	Sequence 2, Appl1	659	64.5	5.4	3033	1	US-07-925-695-8	Sequence 8, Appl1
587	65	5.4	415	4	US-09-799-978-2	Sequence 2, Appl1	660	64.5	5.4	106	4	US-09-370-767-56373	Sequence 56373, A
588	65	5.4	415	4	US-09-799-978-4	Sequence 4, Appl1	661	64	5.4	106	4	US-09-370-767-56373	Sequence 56373, A
589	65	5.4	415	4	US-09-799-978-40	Sequence 40, Appl1	662	64	5.4	168	4	US-09-543-681A-6129	Sequence 6129, Ap
590	65	5.4	415	4	US-09-826-509-483	Sequence 483, App	663	64	5.4	184	4	US-09-448-767A-17465	Sequence 17465, A
591	65	5.4	432	4	US-09-710-279-780	Sequence 780, App	664	64	5.4	216	4	US-09-270-767-46297	Sequence 46297, A
592	65	5.4	441	4	US-09-540-236-2016	Sequence 2016, App	665	64	5.4	284	4	US-09-270-767-52943	Sequence 52943, A
593	65	5.4	461	2	US-08-672-814D-2	Sequence 2, Appl1	666	64	5.4	284	4	US-09-270-767-52943	Sequence 52943, A
594	65	5.4	461	2	US-09-313-696-2	Sequence 2, Appl1	667	64	5.4	285	4	US-09-248-796A-14187	Sequence 14187, A
595	65	5.4	461	3	US-09-282-218A-2	Sequence 2, Appl1	668	64	5.4	226	3	US-09-100-804-12	Sequence 12, Appl1
596	65	5.4	463	3	US-08-612-973-46	Sequence 46, Appl1	669	64	5.4	335	4	US-09-107-532A-4900	Sequence 4900, Ap
597	65	5.4	463	3	US-08-927-597-46	Sequence 46, Appl1	670	64	5.4	336	4	US-09-448-294-5	Sequence 5, Appl1
598	65	5.4	450	3	US-08-612-973-36	Sequence 36, Appl1	671	64	5.4	331	3	US-08-688-988-28	Sequence 28, Appl1
599	65	5.4	450	3	US-08-927-597-36	Sequence 36, Appl1	672	64	5.4	337	4	US-09-489-039A-10505	Sequence 10505, A
600	65	5.4	491	4	US-09-181-339-7	Sequence 7, Appl1	673	64	5.4	333	4	US-09-248-796A-19011	Sequence 19011, A
601	65	5.4	516	4	US-09-949-016-11229	Sequence 11229, A	674	64	5.4	324	4	US-09-489-039A-8361	Sequence 8361, Ap
602	65	5.4	637	4	US-09-543-681A-5869	Sequence 5869, Ap	675	64	5.4	337	3	US-09-134-001C-4802	Sequence 4802, Ap
603	65	5.4	692	3	US-08-612-973-48	Sequence 48, Appl1	676	64	5.4	411	1	US-08-811-897A-12	Sequence 12, Appl1
604	65	5.4	692	3	US-08-927-597-48	Sequence 48, Appl1	677	64	5.4	411	3	US-08-981-189B-18	Sequence 18, Appl1
605	65	5.4	809	3	US-08-612-973-50	Sequence 50, Appl1	678	64	5.4	411	4	US-09-799-978-18	Sequence 18, Appl1
606	65	5.4	809	3	US-08-927-597-50	Sequence 50, Appl1	679	64	5.4	411	4	US-09-881-401-4	Sequence 4, Appl1
607	65	5.4	1033	4	US-09-328-352-5138	Sequence 5138, Ap	680	64	5.4	412	4	US-09-491-577-72	Sequence 72, Appl1
608	64.5	5.4	215	4	US-09-107-532A-3730	Sequence 3730, Ap	681	64	5.4	413	4	US-09-540-236-2393	Sequence 2393, Ap
609	64.5	5.4	263	1	US-08-565-386-9	Sequence 9, Appl1	682	64	5.4	416	4	US-09-583-447A-6	Sequence 6, Appl1
610	64.5	5.4	271	4	US-09-328-352-7066	Sequence 7066, Ap	683	64	5.4	420	4	US-08-981-189B-13	Sequence 13, Appl1
611	64.5	5.4	311	4	US-09-252-991A-17395	Sequence 17395, A	684	64	5.4	431	3		

685	64	5.4	431	4	US-09-799-978-20	Sequence 20, Appl	758	63.5	5.3	409	4	US-09-326-203A-23	Sequence 23, Appl
686	64	5.4	431	4	US-09-881-401-2	Sequence 2, Appl1	759	63.5	5.3	416	4	US-09-328-352-43300	Sequence 4300, Ap
687	64	5.4	448	4	US-09-282-991A-23910	Sequence 23910, A	760	63.5	5.3	428	4	US-09-799-978-36	Sequence 36, Appl
688	64	5.4	469	4	US-09-328-352-4250	Sequence 4250, Ap	761	63.5	5.3	437	4	US-09-949-016-8094	Sequence 8094, Ap
689	64	5.4	469	2	US-09-062-890-38	Sequence 38, Appl	762	63.5	5.3	446	2	US-08-672-814D-11	Sequence 11, Appl
690	64	5.4	501	4	US-09-902-540-11195	Sequence 11195, A	763	63.5	5.3	446	3	US-09-533-696-11	Sequence 11, Appl
691	64	5.4	503	4	US-09-583-447A-2	Sequence 2, Appl1	764	63.5	5.3	446	4	US-09-282-218A-19	Sequence 19, Appl
692	64	5.4	504	4	US-09-583-447A-4	Sequence 4, Appl1	765	63.5	5.3	458	4	US-09-252-991A-20655	Sequence 20655, A
693	64	5.4	534	4	US-09-710-379-920	Sequence 920, App	766	63.5	5.3	474	4	US-09-489-039A-10432	Sequence 10432, A
694	64	5.4	555	4	US-09-543-681A-4582	Sequence 4582, Ap	767	63.5	5.3	483	1	US-08-194-338-7	Sequence 7, Appl1
695	64	5.4	586	3	US-09-040-725A-1	Sequence 1, Appl1	768	63.5	5.3	518	4	US-09-543-681A-4849	Sequence 4849, Ap
696	64	5.4	686	4	US-09-134-000C-5066	Sequence 5066, Ap	769	63.5	5.3	568	4	US-09-469-200E-10	Sequence 10, Appl
697	64	5.4	757	4	US-09-585-858-23	Sequence 23, Appl	770	63.5	5.3	759	2	US-08-637-759E-89	Sequence 89, Appl
698	64	5.4	757	1	US-10-270-878-23	Sequence 23, Appl1	771	63.5	5.3	759	3	US-08-871-355A-89	Sequence 89, Appl
699	64	5.4	967	4	US-08-188-281B-13	Sequence 13, Appl1	772	63.5	5.3	759	3	US-09-201-945-89	Sequence 89, Appl
700	64	5.4	967	5	PCT-US94-07280-13	Sequence 13, Appl	773	63.5	5.3	866	3	US-08-651-999A-1	Sequence 1, Appl1
701	64	5.4	967	5	PCT-US95-01087-13	Sequence 13, Appl	774	63.5	5.3	866	3	US-09-385-752-1	Sequence 1, Appl1
702	64	5.4	1116	4	US-09-543-681A-4379	Sequence 4379, Ap	775	63.5	5.3	2000	4	US-09-382-552-2	Sequence 2, Appl1
703	64	5.4	1462	3	US-07-792-600-31	Sequence 31, Appl	776	63	5.3	147	4	US-09-470-767-45186	Sequence 45186, A
704	64	5.4	1462	3	US-09-157-021-31	Sequence 31, Appl	777	63	5.3	177	4	US-09-492-308A-20	Sequence 20, Appl
705	64	5.4	1462	3	US-09-156-842-31	Sequence 31, Appl	778	63	5.3	180	4	US-09-107-532A-5495	Sequence 5495, Ap
706	64	5.4	1462	4	US-09-591-514-31	Sequence 31, Appl	779	63	5.3	197	4	US-09-198-452A-403	Sequence 403, App
707	64	5.4	1648	1	US-08-188-281B-12	Sequence 12, Appl	780	63	5.3	218	4	US-09-134-001C-4489	Sequence 4489, Ap
708	64	5.4	1648	5	PCT-US94-07280-12	Sequence 12, Appl	781	63	5.3	233	3	US-09-134-001C-4013	Sequence 4013, Ap
709	64	5.4	1648	5	PCT-US94-01087-12	Sequence 12, Appl	782	63	5.3	240	4	US-09-452-991A-29766	Sequence 29766, A
710	64	5.4	2436	3	US-08-444-818-75	Sequence 75, Appl	783	63	5.3	245	4	US-09-949-016-11068	Sequence 11068, A
711	64	5.4	2772	3	US-08-444-818-89	Sequence 89, Appl	784	63	5.3	259	3	US-09-261-599A-3	Sequence 3, Appl1
712	64	5.4	3011	1	US-08-188-281B-1	Sequence 1, Appl1	785	63	5.3	259	4	US-09-456-455A-3	Sequence 3, Appl1
713	64	5.4	3011	1	US-08-453-552-1	Sequence 1, Appl1	786	63	5.3	264	4	US-09-270-767-41787	Sequence 41787, A
714	64	5.4	3011	2	US-08-710-637-1	Sequence 1, Appl1	787	63	5.3	295	4	US-09-583-110-4171	Sequence 4171, Ap
715	64	5.4	3011	5	PCT-US93-00907-1	Sequence 1, Appl1	788	63	5.3	299	4	US-09-107-532A-5499	Sequence 5499, Ap
716	64	5.4	3011	5	PCT-US94-07280-1	Sequence 1, Appl1	789	63	5.3	353	3	US-09-134-001C-3246	Sequence 3246, Ap
717	64	5.4	3011	5	PCT-US95-01087-1	Sequence 1, Appl1	790	63	5.3	359	3	US-08-688-988-32	Sequence 32, Appl
718	64	5.3	118	3	US-09-627-376-17	Sequence 17, Appl	791	63	5.3	361	1	US-08-390-162-4	Sequence 4, Appl1
719	63.5	5.3	118	4	US-10-047-676B-17	Sequence 17, Appl	792	63	5.3	361	1	US-08-685-945B-4	Sequence 4, Appl1
720	63.5	5.3	124	4	US-09-270-767-54829	Sequence 34829, A	793	63	5.3	365	1	US-08-390-162-2	Sequence 2, Appl1
721	63.5	5.3	124	4	US-09-270-767-50046	Sequence 50046, A	794	63	5.3	365	1	US-08-685-945B-2	Sequence 2, Appl1
722	63.5	5.3	134	4	US-09-513-999C-6305	Sequence 6305, Ap	795	63	5.3	366	4	US-09-107-433-5158	Sequence 5158, Ap
723	63.5	5.3	209	4	US-09-134-000C-3922	Sequence 3922, Ap	796	63	5.3	370	3	US-09-172-353-2	Sequence 2, Appl1
724	63.5	5.3	219	4	US-09-270-767-41489	Sequence 41489, A	797	63	5.3	370	3	US-09-172-353-3	Sequence 3, Appl1
725	63.5	5.3	228	4	US-09-107-433-3974	Sequence 3974, Ap	798	63	5.3	370	4	US-09-799-955-2	Sequence 2, Appl1
726	63.5	5.3	253	4	US-09-602-787A-8	Sequence 8, Appl1	799	63	5.3	370	4	US-09-799-955-3	Sequence 3, Appl1
727	63.5	5.3	264	4	US-09-489-039A-9738	Sequence 9738, Ap	800	63	5.3	383	4	US-09-710-279-2446	Sequence 2426, Ap
728	63.5	5.3	275	1	US-08-118-270-66	Sequence 66, Appl	801	63	5.3	384	3	US-09-134-001C-3437	Sequence 3437, Ap
729	63.5	5.3	275	5	PCT-US93-08528-66	Sequence 66, Appl	802	63	5.3	415	3	US-08-482-746-13	Sequence 13, Appl
730	63.5	5.3	279	3	US-09-134-001C-4667	Sequence 4667, Ap	803	63	5.3	415	4	US-09-580-734-13	Sequence 13, Appl
731	63.5	5.3	280	1	US-08-781-562-4	Sequence 4, Appl1	804	63	5.3	415	4	US-08-374-009-13	Sequence 13, Appl
732	63.5	5.3	308	4	US-09-252-991A-16800	Sequence 16800, A	805	63	5.3	415	4	US-09-191-724-13	Sequence 13, Appl
733	63.5	5.3	342	3	US-09-116-498-4	Sequence 4, Appl1	806	63	5.3	415	4	US-09-199-978-22	Sequence 22, Appl
734	63.5	5.3	342	3	US-09-116-498-6	Sequence 6, Appl1	807	63	5.3	422	3	US-09-625-188-12	Sequence 12, Appl
735	63.5	5.3	342	4	US-09-852-156-4	Sequence 6, Appl1	808	63	5.3	431	1	US-08-581-433A-2	Sequence 2, Appl1
736	63.5	5.3	342	4	US-09-852-156-6	Sequence 6, Appl1	809	63	5.3	441	1	US-09-489-039A-10091	Sequence 10091, A
737	63.5	5.3	349	4	US-09-252-991A-24644	Sequence 24644, A	810	63	5.3	450	1	US-08-194-338-5	Sequence 5, Appl1
738	63.5	5.3	350	4	US-09-556-002-2	Sequence 2, Appl1	811	63	5.3	450	1	US-08-444-734A-8	Sequence 8, Appl1
739	63.5	5.3	358	4	US-09-270-767-41449	Sequence 41449, A	812	63	5.3	451	3	US-09-134-001C-4420	Sequence 4420, Ap
740	63.5	5.3	365	4	US-09-933-999A-5	Sequence 5, Appl1	813	63	5.3	489	2	US-09-062-890-34	Sequence 34, Appl
741	63.5	5.3	372	1	US-08-202-056-5	Sequence 5, Appl1	814	63	5.3	489	2	US-09-062-890-36	Sequence 36, Appl
742	63.5	5.3	372	1	US-08-076-093A-6	Sequence 6, Appl1	815	63	5.3	509	2	US-08-890-980-2	Sequence 2, Appl1
743	63.5	5.3	372	1	US-08-701-265-6	Sequence 6, Appl1	816	63	5.3	509	3	US-08-890-979-2	Sequence 2, Appl1
744	63.5	5.3	372	2	US-08-284-586-6	Sequence 6, Appl1	817	63	5.3	509	3	US-09-031-626-2	Sequence 2, Appl1
745	63.5	5.3	372	2	US-08-805-478-6	Sequence 6, Appl1	818	63	5.3	509	3	US-09-032-894-2	Sequence 2, Appl1
746	63.5	5.3	372	2	US-08-802-627A-6	Sequence 6, Appl1	819	63	5.3	509	4	US-09-054-272-59	Sequence 29, Appl
747	63.5	5.3	372	2	US-08-801-238-6	Sequence 6, Appl1	820	63	5.3	640	4	US-09-552-991A-27542	Sequence 27542, A
748	63.5	5.3	372	2	US-08-801-328-6	Sequence 6, Appl1	821	63	5.3	692	4	US-09-540-236-3150	Sequence 3150, Ap
749	63.5	5.3	372	3	US-08-104-296-6	Sequence 6, Appl1	822	63	5.3	729	3	US-09-291-922-29	Sequence 29, Appl
750	63.5	5.3	372	3	US-08-962-493-8	Sequence 8, Appl1	823	63	5.3	795	4	US-09-252-991A-19085	Sequence 19085, A
751	63.5	5.3	372	4	US-09-170-496D-66	Sequence 66, Appl	824	63	5.3	822	4	US-08-684-932A-38	Sequence 38, Appl
752	63.5	5.3	372	4	US-09-170-496D-200	Sequence 200, App	825	63	5.3	822	4	US-09-618-308A-2	Sequence 2, Appl1
753	63.5	5.3	378	4	US-09-949-016-10255	Sequence 10255, A	826	63	5.3	923	2	US-08-469-537A-107	Sequence 107, App
754	63.5	5.3	379	4	US-09-248-796A-14491	Sequence 14491, A	827	63	5.3	1027	4	US-09-902-540-11750	Sequence 11750, A
755	63.5	5.3	397	4	US-09-583-110-2946	Sequence 2946, Ap	828	63	5.3	1802	3	US-09-322-478-18	Sequence 18, Appl
756	63.5	5.3	404	4	US-09-107-433-3747	Sequence 3747, Ap	829	63	5.3	1802	4	US-09-586-106D-18	Sequence 18, Appl
757	63.5	5.3	406	4	US-09-252-991A-26429	Sequence 26429, A	830	62.5	5.2	80	4	US-09-248-796A-26578	Sequence 26578, A

831	62.5	5.2	136	2	US-08-477-451-31	Sequence 31, Appl	904	62	5.2	272	4	US-09-303-456-81	Sequence 81, Appl
832	62.5	5.2	140	4	US-09-270-767-60416	Sequence 40416, A	905	62	5.2	280	4	US-09-302-540-10330	Sequence 10330, A
833	62.5	5.2	140	4	US-09-270-767-55632	Sequence 55632, A	906	62	5.2	283	4	US-09-303-456-88	Sequence 88, Appl
834	62.5	5.2	161	3	US-09-413-814-15	Sequence 15, Appl	907	62	5.2	288	4	US-09-303-456-84	Sequence 84, Appl
835	62.5	5.2	183	4	US-09-107-532A-7197	Sequence 7197, Ap	908	62	5.2	290	3	US-09-134-001C-4893	Sequence 4893, Ap
836	62.5	5.2	191	4	US-09-270-767-40648	Sequence 40648, A	909	62	5.2	292	4	US-09-303-456-82	Sequence 82, Appl
837	62.5	5.2	191	4	US-09-270-767-55864	Sequence 55864, A	910	62	5.2	295	4	US-09-303-456-86	Sequence 86, Appl
838	62.5	5.2	197	4	US-09-486-147-40	Sequence 40, Appl	911	62	5.2	305	4	US-09-270-767-44944	Sequence 44944, A
839	62.5	5.2	200	4	US-09-270-767-6009	Sequence 36009, A	912	62	5.2	317	4	US-09-489-039A-9602	Sequence 9602, Ap
840	62.5	5.2	200	4	US-09-270-767-51226	Sequence 51226, A	913	62	5.2	333	1	US-07-667-276A-7	Sequence 7, Appl
841	62.5	5.2	214	4	US-09-710-279-774	Sequence 714, App	914	62	5.2	336	4	US-09-543-681A-7161	Sequence 7161, Ap
842	62.5	5.2	221	4	US-09-248-796A-15088	Sequence 15088, A	915	62	5.2	331	2	US-08-560-098A-46	Sequence 46, Appl
843	62.5	5.2	252	4	US-09-270-767-45203	Sequence 45203, A	916	62	5.2	335	1	US-07-759-568-1	Sequence 1, Appl
844	62.5	5.2	261	4	US-09-328-352-6619	Sequence 6619, Ap	917	62	5.2	335	1	US-08-450-393A-8	Sequence 8, Appl
845	62.5	5.2	304	4	US-09-252-991A-22398	Sequence 22398, A	918	62	5.2	335	2	US-08-390-000A-5	Sequence 5, Appl
846	62.5	5.2	304	4	US-09-107-532A-4681	Sequence 4681, Ap	919	62	5.2	335	3	US-08-446-669-8	Sequence 8, Appl
847	62.5	5.2	327	2	US-08-926-724-1	Sequence 1, Appl	920	62	5.2	335	3	US-09-045-583-53	Sequence 53, Appl
848	62.5	5.2	327	4	US-09-949-016-6562	Sequence 6562, Ap	921	62	5.2	335	4	US-09-534-185-53	Sequence 53, Appl
849	62.5	5.2	341	4	US-09-252-991A-30051	Sequence 30051, A	922	62	5.2	335	4	US-09-625-573-8	Sequence 8, Appl
850	62.5	5.2	342	4	US-09-134-000C-5123	Sequence 5123, Ap	923	62	5.2	335	5	PCT-US95-00476-8	Sequence 8, Appl
851	62.5	5.2	343	4	US-09-743-871B-1	Sequence 714, Ap	924	62	5.2	360	1	US-08-202-056-7	Sequence 7, Appl
852	62.5	5.2	343	4	US-09-743-871B-5	Sequence 5, Appl	925	62	5.2	360	1	US-08-597-236-11	Sequence 11, Appl
853	62.5	5.2	345	4	US-09-543-681A-4410	Sequence 4410, Ap	926	62	5.2	360	1	US-08-746-682A-11	Sequence 11, Appl
854	62.5	5.2	349	3	US-09-162-524-3	Sequence 3, Appl	927	62	5.2	360	4	US-09-409-778-4	Sequence 4, Appl
855	62.5	5.2	349	4	US-09-762-661A-2	Sequence 2, Appl	928	62	5.2	361	4	US-09-710-279-184	Sequence 184, Ap
856	62.5	5.2	353	4	US-09-949-016-8077	Sequence 8077, Ap	929	62	5.2	384	4	US-09-491-577-16	Sequence 16, Appl
857	62.5	5.2	383	4	US-09-330-335-8	Sequence 8, Appl	930	62	5.2	383	4	US-09-252-991A-25633	Sequence 25633, A
858	62.5	5.2	383	5	PCT-US94-01321-2	Sequence 2, Appl	931	62	5.2	405	4	US-09-489-039A-7574	Sequence 7574, Ap
859	62.5	5.2	432	4	US-09-489-039A-7223	Sequence 7223, Ap	932	62	5.2	407	4	US-09-949-016-11348	Sequence 11348, A
860	62.5	5.2	434	4	US-09-198-452A-434	Sequence 434, App	933	62	5.2	409	4	US-09-583-110-3749	Sequence 3749, Ap
861	62.5	5.2	434	4	US-09-438-185A-417	Sequence 417, App	934	62	5.2	412	3	US-09-134-001C-3949	Sequence 3949, Ap
862	62.5	5.2	439	4	US-09-489-039A-13336	Sequence 13336, A	935	62	5.2	413	4	US-09-107-433-2887	Sequence 2887, Ap
863	62.5	5.2	441	4	US-09-248-796A-16114	Sequence 16114, A	936	62	5.2	414	4	US-09-198-452A-414	Sequence 414, App
864	62.5	5.2	442	3	US-08-121-446-4	Sequence 4, Appl	937	62	5.2	414	4	US-09-438-185A-396	Sequence 396, App
865	62.5	5.2	442	4	US-09-520-210-10	Sequence 10, Appl	938	62	5.2	415	4	US-09-799-978-28	Sequence 28, Appl
866	62.5	5.2	442	4	US-09-826-509-497	Sequence 497, App	939	62	5.2	417	4	US-09-710-279-950	Sequence 950, App
867	62.5	5.2	443	3	US-09-161-994A-3	Sequence 3, Appl	940	62	5.2	447	4	US-09-388-089B-2	Sequence 2, Appl
868	62.5	5.2	452	1	US-08-117-361C-1	Sequence 1, Appl	941	62	5.2	473	1	US-08-597-236-13	Sequence 13, Appl
869	62.5	5.2	452	4	US-09-710-279-1834	Sequence 1834, Ap	942	62	5.2	473	1	US-08-746-682A-13	Sequence 13, Appl
870	62.5	5.2	453	4	US-09-489-039A-10468	Sequence 10468, A	943	62	5.2	475	4	US-09-388-089B-12	Sequence 12, Appl
871	62.5	5.2	453	4	US-09-769-863-14	Sequence 14, Appl	944	62	5.2	489	1	US-08-589-893-22	Sequence 22, Appl
872	62.5	5.2	459	4	US-09-489-039A-9027	Sequence 9027, Ap	945	62	5.2	489	1	US-08-589-893-14	Sequence 14, Appl
873	62.5	5.2	463	3	US-09-134-001C-3973	Sequence 3973, Ap	946	62	5.2	489	1	US-08-589-893-24	Sequence 24, Appl
874	62.5	5.2	463	4	US-09-489-039A-13646	Sequence 13646, A	947	62	5.2	489	2	US-09-020-991-14	Sequence 14, Appl
875	62.5	5.2	480	4	US-09-489-039A-13045	Sequence 13045, A	948	62	5.2	489	2	US-09-020-991-22	Sequence 22, Appl
876	62.5	5.2	539	4	US-09-949-016-6363	Sequence 6363, Ap	949	62	5.2	489	2	US-09-020-991-24	Sequence 24, Appl
877	62.5	5.2	541	3	US-09-158-767-19	Sequence 19, Appl	950	62	5.2	489	2	US-09-062-890-14	Sequence 14, Appl
878	62.5	5.2	541	3	US-09-158-767-20	Sequence 20, Appl	951	62	5.2	489	2	US-09-062-890-22	Sequence 22, Appl
879	62.5	5.2	541	4	US-09-713-794-19	Sequence 19, Appl	952	62	5.2	489	2	US-09-062-890-24	Sequence 24, Appl
880	62.5	5.2	541	4	US-09-713-794-30	Sequence 30, Appl	953	62	5.2	488	4	US-09-388-089B-11	Sequence 11, Appl
881	62.5	5.2	557	1	US-08-424-788-6	Sequence 6, Appl	954	62	5.2	489	4	US-09-673-898-6	Sequence 6, Appl
882	62.5	5.2	578	1	US-08-424-788-5	Sequence 5, Appl	955	62	5.2	567	3	US-09-560-639-7	Sequence 7, Appl
883	62.5	5.2	578	1	US-08-110-683-2	Sequence 2, Appl	956	62	5.2	567	3	US-09-173-151A-24	Sequence 24, Appl
884	62.5	5.2	578	1	US-08-683-743-2	Sequence 2, Appl	957	62	5.2	567	3	US-09-032-337-39	Sequence 39, Appl
885	62.5	5.2	578	2	US-08-477-166-2	Sequence 2, Appl	958	62	5.2	582	3	US-08-194-560-2	Sequence 2, Appl
886	62.5	5.2	578	2	US-08-472-097-2	Sequence 2, Appl	959	62	5.2	602	3	US-09-134-001C-4416	Sequence 4416, Ap
887	62.5	5.2	578	4	US-09-439-672-2	Sequence 2, Appl	960	62	5.2	638	3	US-09-376-781-6	Sequence 6, Appl
888	62.5	5.2	578	5	PCT-US93-11638-2	Sequence 2, Appl	961	62	5.2	706	4	US-09-538-092-957	Sequence 957, App
889	62.5	5.2	605	4	US-09-328-352-7890	Sequence 7890, Ap	962	62	5.2	747	4	US-09-949-016-10040	Sequence 10040, A
890	62.5	5.2	628	4	US-09-107-532A-5288	Sequence 5288, Ap	963	62	5.2	775	3	US-09-305-640-2	Sequence 2, Appl
891	62.5	5.2	669	3	US-09-342-647-18	Sequence 18, Appl	964	62	5.2	800	4	US-09-248-796A-20101	Sequence 20101, A
892	62.5	5.2	765	4	US-09-134-000C-6690	Sequence 6690, Ap	965	62	5.2	1186	1	US-08-602-737-6	Sequence 6, Appl
893	62.5	5.2	796	4	US-09-270-767-40617	Sequence 40617, Ap	966	62	5.2	1186	3	US-09-001-982-6	Sequence 6, Appl
894	62.5	5.2	796	4	US-09-270-767-55833	Sequence 55833, A	967	62	5.2	1186	4	US-09-668-650-6	Sequence 6, Appl
895	62.5	5.2	1414	4	US-09-902-540-10957	Sequence 10957, A	968	62	5.2	1287	4	US-09-543-681A-6130	Sequence 6130, Ap
896	62.5	5.2	1768	4	US-09-489-039A-11704	Sequence 11704, A	969	62	5.2	1985	4	US-09-949-016-8171	Sequence 8171, Ap
897	62	5.2	91	4	US-09-248-796A-23462	Sequence 23462, A	970	61.5	5.1	130	4	US-09-543-681A-6130	Sequence 6130, Ap
898	62	5.2	112	4	US-09-270-767-59183	Sequence 59183, A	971	61.5	5.1	163	3	US-08-600-430-4	Sequence 4, Appl
899	62	5.2	129	4	US-09-673-898-10	Sequence 10, Appl	972	61.5	5.1	170	4	US-09-710-279-1164	Sequence 1164, Ap
900	62	5.2	250	4	US-09-270-767-43784	Sequence 43784, A	973	61.5	5.1	186	3	US-09-134-001C-40995	Sequence 4095, Ap
901	62	5.2	254	4	US-09-248-796A-22532	Sequence 22532, A	974	61.5	5.1	188	4	US-09-902-540-11995	Sequence 11995, A
902	62	5.2	272	4	US-09-903-456-76	Sequence 76, Appl	975	61.5	5.1	235	3	US-08-812-586-16	Sequence 16, Appl
903	62	5.2	272	4	US-09-903-456-80	Sequence 80, Appl	976	61.5	5.1	235	4	US-09-535-832A-17	Sequence 17, Appl

977	61.5	5.1	260	4	US-09-540-236-3812	Sequence 3812, Ap	1050	61.5	5.1	2247	4	US-09-660-541-2	Sequence 2, Appl1
978	61.5	5.1	269	4	US-09-489-039A-9180	Sequence 9180, Ap	1051	61.5	5.1	3066	3	US-08-952-127-12	Sequence 12, Appl1
979	61.5	5.1	271	3	US-09-077-675A-12	Sequence 12, Appl	1052	61	5.1	95	4	US-09-248-796A-21665	Sequence 21665, A
980	61.5	5.1	271	4	US-09-077-674-12	Sequence 1271, Appl	1053	61	5.1	122	4	US-09-710-279-102	Sequence 102, App
981	61.5	5.1	288	4	US-09-134-000C-5520	Sequence 5520, Ap	1054	61	5.1	175	2	US-08-408-095-11	Sequence 11, Appl
982	61.5	5.1	289	4	US-09-489-039A-12390	Sequence 12390, A	1055	61	5.1	188	4	US-09-198-452A-1206	Sequence 1206, Ap
983	61.5	5.1	297	4	US-09-328-352-5769	Sequence 5769, Ap	1056	61	5.1	199	3	US-09-080-643-4	Sequence 4, Appl1
984	61.5	5.1	302	3	US-09-077-675A-2	Sequence 2, Appl1	1057	61	5.1	200	4	US-09-710-279-394	Sequence 394, Appl1
985	61.5	5.1	302	3	US-09-077-675A-7	Sequence 7, Appl1	1058	61	5.1	200	4	US-09-710-279-1242	Sequence 1242, Ap
986	61.5	5.1	302	4	US-09-077-674-2	Sequence 2, Appl1	1059	61	5.1	202	4	US-08-657-749D-17	Sequence 17, Appl
987	61.5	5.1	302	4	US-09-077-674-7	Sequence 7, Appl1	1060	61	5.1	206	3	US-09-134-001C-3929	Sequence 3929, Ap
988	61.5	5.1	343	4	US-09-543-681A-6853	Sequence 6853, Ap	1061	61	5.1	207	3	US-08-559-397A-13	Sequence 13, Appl1
989	61.5	5.1	349	4	US-09-270-767-38347	Sequence 38347, A	1062	61	5.1	209	3	US-08-559-397A-11	Sequence 11, Appl
990	61.5	5.1	349	4	US-09-270-767-53564	Sequence 53564, A	1063	61	5.1	225	4	US-09-252-991A-30213	Sequence 30213, A
991	61.5	5.1	353	3	US-09-077-675A-3	Sequence 3, Appl1	1064	61	5.1	220	3	US-09-134-001C-3744	Sequence 3744, Ap
992	61.5	5.1	353	4	US-09-077-674-3	Sequence 3, Appl1	1065	61	5.1	239	4	US-09-710-279-978	Sequence 978, App
993	61.5	5.1	361	3	US-09-077-675A-8	Sequence 8, Appl1	1066	61	5.1	241	4	US-09-489-039A-83397	Sequence 8397, Ap
994	61.5	5.1	361	4	US-09-077-674-8	Sequence 8, Appl1	1067	61	5.1	266	1	US-08-236-918A-6	Sequence 6, Appl1
995	61.5	5.1	366	3	US-09-077-675A-13	Sequence 13, Appl	1068	61	5.1	266	3	US-09-150-864A-6	Sequence 6, Appl1
996	61.5	5.1	366	4	US-09-077-674-13	Sequence 13, Appl	1069	61	5.1	266	4	US-08-012-269A-2	Sequence 2, Appl1
997	61.5	5.1	366	4	US-09-170-496D-88	Sequence 88, Appl	1070	61	5.1	266	4	US-09-623-545A-3	Sequence 3, Appl1
998	61.5	5.1	366	4	US-09-743-742B-7	Sequence 7, Appl1	1071	61	5.1	266	5	PCT-US96-0396S-2	Sequence 2, Appl1
999	61.5	5.1	366	4	US-09-762-661A-5	Sequence 5, Appl1	1072	61	5.1	261	3	US-09-107-532A-6716	Sequence 3485, Ap
1000	61.5	5.1	366	4	US-09-762-661A-5	Sequence 7, Appl1	1073	61	5.1	265	4	US-09-107-532A-6716	Sequence 6716, Ap
1001	61.5	5.1	366	4	US-09-364-425B-45	Sequence 45, Appl1	1074	61	5.1	272	4	US-09-903-456-78	Sequence 78, Appl
1002	61.5	5.1	366	4	US-09-743-475-4	Sequence 4, Appl1	1075	61	5.1	277	4	US-09-583-110-3171	Sequence 3171, Ap
1003	61.5	5.1	366	4	US-09-743-475-6	Sequence 6, Appl1	1076	61	5.1	279	4	US-09-107-433-3691	Sequence 3691, Ap
1004	61.5	5.1	376	2	US-08-465-976A-3	Sequence 3, Appl1	1077	61	5.1	281	4	US-10-121-857-45	Sequence 45, Appl1
1005	61.5	5.1	376	2	US-08-982-412-3	Sequence 3, Appl1	1078	61	5.1	285	4	US-09-543-681A-7666	Sequence 7666, Ap
1006	61.5	5.1	376	4	US-09-107-433-3823	Sequence 3823, Ap	1079	61	5.1	286	4	US-09-540-236-2583	Sequence 2583, Ap
1007	61.5	5.1	379	3	US-09-740-035-4	Sequence 4, Appl1	1080	61	5.1	288	4	US-09-438-185A-545	Sequence 545, App
1008	61.5	5.1	391	1	US-07-921-178A-2	Sequence 2, Appl1	1081	61	5.1	302	4	US-08-311-731A-173	Sequence 173, App
1009	61.5	5.1	391	1	US-08-103-445-5	Sequence 5, Appl1	1082	61	5.1	338	4	US-09-107-532A-6222	Sequence 6222, Ap
1010	61.5	5.1	391	2	US-08-461-690B-5	Sequence 5, Appl1	1083	61	5.1	345	4	US-09-107-532A-5817	Sequence 5817, Ap
1011	61.5	5.1	391	2	US-08-501-003A-16	Sequence 16, Appl	1084	61	5.1	345	4	US-09-489-039A-7417	Sequence 7417, Ap
1012	61.5	5.1	392	4	US-09-275-252A-13	Sequence 13, Appl	1085	61	5.1	355	4	US-08-833-752-8	Sequence 8, Appl1
1013	61.5	5.1	392	4	US-09-489-039A-8713	Sequence 8713, Ap	1086	61	5.1	355	4	US-09-938-719-8	Sequence 8, Appl1
1014	61.5	5.1	397	4	US-08-741-134-6	Sequence 6, Appl1	1087	61	5.1	358	4	US-09-939-826B-8	Sequence 8, Appl1
1015	61.5	5.1	411	2	US-08-981-189B-10	Sequence 10, Appl	1088	61	5.1	385	4	US-09-248-796A-19081	Sequence 19081, A
1016	61.5	5.1	415	3	US-08-981-189B-10	Sequence 6, Appl1	1089	61	5.1	385	3	US-08-688-988-30	Sequence 30, Appl
1017	61.5	5.1	415	3	US-08-482-746-6	Sequence 6, Appl1	1090	61	5.1	408	4	US-09-328-352-5768	Sequence 5768, Ap
1018	61.5	5.1	415	3	US-09-580-734-6	Sequence 6, Appl1	1091	61	5.1	440	4	US-09-799-978-34	Sequence 34, Appl
1019	61.5	5.1	415	4	US-08-374-009-6	Sequence 6, Appl1	1092	61	5.1	445	4	US-09-248-796A-16683	Sequence 16683, A
1020	61.5	5.1	415	4	US-09-191-724-6	Sequence 6, Appl1	1093	61	5.1	481	4	US-09-489-039A-15101	Sequence 15101, A
1021	61.5	5.1	415	4	US-09-799-978-16	Sequence 16, Appl	1094	61	5.1	489	4	US-09-710-279-2632	Sequence 2632, Ap
1022	61.5	5.1	415	4	US-09-252-991A-26638	Sequence 26638, A	1095	61	5.1	500	4	US-09-134-000C-4886	Sequence 4886, Ap
1023	61.5	5.1	418	4	US-09-543-681A-7634	Sequence 7634, Ap	1096	61	5.1	503	3	US-09-949-016-6469	Sequence 3948, Ap
1024	61.5	5.1	427	4	US-09-942-501-2	Sequence 2, Appl1	1097	61	5.1	535	4	US-09-949-016-6469	Sequence 6469, Ap
1025	61.5	5.1	458	4	US-09-252-991A-28897	Sequence 28897, A	1098	61	5.1	558	4	US-09-949-016-7736	Sequence 26, Appl
1026	61.5	5.1	469	4	US-08-956-171B-5245	Sequence 5245, Ap	1099	61	5.1	672	4	US-09-556-916-26	Sequence 28, Appl
1027	61.5	5.1	469	4	US-08-781-986A-5245	Sequence 5245, Ap	1100	61	5.1	672	4	US-09-556-916-28	Sequence 30228, A
1028	61.5	5.1	479	2	US-08-899-514-2	Sequence 2, Appl1	1101	61	5.1	724	4	US-09-252-991A-30228	Sequence 6, Appl1
1029	61.5	5.1	497	1	US-08-295-670-6	Sequence 6, Appl1	1102	61	5.1	732	4	US-10-160-748-6	Sequence 14319, A
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1031	61.5	5.1	524	3	US-09-134-001C-3368	Sequence 3368, Ap	1104	61	5.1	766	4	US-09-489-039A-17109	Sequence 13, Appl
1032	61.5	5.1	524	2	US-08-853-659A-35	Sequence 35, Appl	1105	61	5.1	806	6	US-09-833-466-13	Sequence 5059, Ap
1033	61.5	5.1	526	1	US-08-298-426-4	Sequence 4, Appl1	1106	61	5.1	815	4	US-09-107-433-3059	Sequence 2738, Ap
1034	61.5	5.1	615	4	US-09-602-787A-534	Sequence 534, App	1107	61	5.1	848	4	US-09-538-092-577	Sequence 577, App
1035	61.5	5.1	615	4	US-09-602-787A-536	Sequence 536, App	1108	61	5.1	880	4	US-09-107-532A-3714	Sequence 3714, App
1036	61.5	5.1	659	4	US-09-583-110-5110	Sequence 5110, App	1109	61	5.1	915	4	US-09-949-016-8301	Sequence 8011, Ap
1037	61.5	5.1	674	4	US-09-538-092-1125	Sequence 1125, Ap	1110	61	5.1	1088	4	US-09-949-016-8301	Sequence 31121, A
1038	61.5	5.1	685	4	US-09-720-317A-31	Sequence 317A, Appl	1111	61	5.1	1299	4	US-09-489-039A-83397	Sequence 8397, Ap
1039	61.5	5.1	692	4	US-09-248-796A-18612	Sequence 18612, A	1112	61	5.1	1336	4	US-09-600-087-2	Sequence 2, Appl1
1040	61.5	5.1	756	4	US-09-949-016-6547	Sequence 6547, Ap	1113	61	5.1	1503	4	US-09-949-016-6341	Sequence 6341, Ap
1041	61.5	5.1	817	1	US-08-381-931B-2	Sequence 2, Appl1	1114	61	5.1	1503	4	US-09-949-016-6341	Sequence 11100, A
1042	61.5	5.1	865	4	US-09-902-540-10416	Sequence 10416, A	1115	61	5.1	1579	4	US-09-949-016-8301	Sequence 8301, Ap
1043	61.5	5.1	895	4	US-09-489-039A-13127	Sequence 13127, A	1116	61	5.1	2079	4	US-08-469-260A-394	Sequence 394, App
1044	61.5	5.1	965	4	US-09-437-277-3	Sequence 3, Appl1	1117	61	5.1	2864	4	US-08-488-446-394	Sequence 394, App
1045	61.5	5.1	1025	4	US-09-543-681A-7112	Sequence 7112, Appl	1118	61	5.1	2864	4	US-08-467-344A-334	Sequence 394, App
1046	61.5	5.1	2232	3	US-09-091-219-25	Sequence 25, Appl	1119	61	5.1	2864	4	US-08-424-550D-334	Sequence 394, App
1047	61.5	5.1	2232	4	US-09-660-541-25	Sequence 25, Appl	1120	61	5.1	3011	3	US-08-811-566-20	Sequence 20, Appl
1048	61.5	5.1	2232	3	US-09-091-219-2	Sequence 2, Appl1	1121	61	5.1				
1049	61.5	5.1	2247	3	US-09-091-219-2	Sequence 2, Appl1	1122	61	5.1				

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1124	61	5.1	3011	3	US-09-034-756-20	Sequence 20, Appl1	1197	60.5	5.1	537	3	US-09-134-001C-4091	Sequence 4091, Ap
1125	61	5.1	3011	4	US-10-104-966-1	Sequence 1, Appl1	1198	60.5	5.1	538	3	US-09-134-001C-5109	Sequence 5109, Ap
1126	61	5.1	3011	4	US-09-952-572-9	Sequence 9, Appl1	1199	60.5	5.1	539	4	US-09-543-681A-5774	Sequence 5774, Ap
1127	61	5.1	3012	3	US-08-811-566-2	Sequence 2, Appl1	1200	60.5	5.1	540	4	US-09-540-236-2943	Sequence 2943, Ap
1128	61	5.1	3012	3	US-09-034-756-2	Sequence 2, Appl1	1201	60.5	5.1	541	4	US-09-595-684B-35	Sequence 35, Appl1
1129	60.5	5.1	73	4	US-09-543-681A-6595	Sequence 6595, Ap	1202	60.5	5.1	682	4	US-09-107-532A-4499	Sequence 4499, Ap
1130	60.5	5.1	107	4	US-09-107-532A-5805	Sequence 5805, Ap	1203	60.5	5.1	684	4	US-09-248-796A-20210	Sequence 20210, A
1131	60.5	5.1	116	4	US-09-270-767-36280	Sequence 36280, A	1204	60.5	5.1	726	4	US-09-107-532A-6007	Sequence 6007, Ap
1132	60.5	5.1	116	4	US-09-270-767-51457	Sequence 51457, A	1205	60.5	5.1	865	4	US-09-612-204B-24	Sequence 24, Appl1
1133	60.5	5.1	157	4	US-09-270-767-32124	Sequence 32124, A	1206	60.5	5.1	1064	4	US-09-248-796A-16640	Sequence 16640, A
1134	60.5	5.1	157	4	US-09-270-767-47341	Sequence 47341, A	1207	60.5	5.1	1225	4	US-09-949-016-9468	Sequence 9468, Ap
1135	60.5	5.1	157	4	US-09-270-767-58298	Sequence 58298, A	1208	60.5	5.1	1333	4	US-09-270-767-46728	Sequence 46728, A
1136	60.5	5.1	159	6	5208144-32	Patent No. 5208144	1209	60.5	5.1	1912	3	US-08-913-832A-2	Sequence 2, Appl1
1137	60.5	5.1	159	6	5208144-32	Patent No. 5208144	1210	60.5	5.1	1912	4	US-09-158-707-2	Sequence 2, Appl1
1138	60.5	5.1	194	4	US-09-270-767-34926	Sequence 34926, A	1211	60.5	5.1	1912	4	US-09-158-707-2	Sequence 2, Appl1
1139	60.5	5.1	194	4	US-09-270-767-50143	Sequence 50143, A	1212	60.5	5.1	5032	4	US-09-338-092-979	Sequence 979, Ap
1140	60.5	5.1	195	4	US-09-612-204B-2	Sequence 2, Appl1	1213	60	5.0	136	4	US-09-270-767-46978	Sequence 31761, A
1141	60.5	5.1	197	4	US-09-270-767-58832	Sequence 58832, A	1214	60	5.0	136	4	US-09-270-767-46978	Sequence 46978, A
1142	60.5	5.1	198	4	US-09-976-451-5	Sequence 5, Appl1	1215	60	5.0	162	4	US-09-134-000C-4993	Sequence 4993, Ap
1143	60.5	5.1	199	3	US-08-478-316-33	Sequence 33, Appl1	1216	60	5.0	177	4	US-09-492-308A-23	Sequence 23, Appl1
1144	60.5	5.1	199	3	US-09-019-793A-33	Sequence 33, Appl1	1217	60	5.0	189	3	US-09-080-643-23	Sequence 2, Appl1
1145	60.5	5.1	200	2	US-08-799-464A-9	Sequence 9, Appl1	1218	60	5.0	189	4	US-09-270-767-32341	Sequence 32341, A
1146	60.5	5.1	200	4	US-09-601-326-33	Sequence 33, Appl1	1219	60	5.0	189	4	US-09-270-767-47558	Sequence 47558, A
1147	60.5	5.1	200	5	PCT-US95-09927-9	Sequence 9, Appl1	1220	60	5.0	191	4	US-09-583-110-3197	Sequence 3197, Ap
1148	60.5	5.1	207	4	US-08-811-519-18	Sequence 18, Appl1	1221	60	5.0	199	4	US-09-107-433-3384	Sequence 3384, Ap
1149	60.5	5.1	222	4	US-09-270-767-42973	Sequence 42973, A	1222	60	5.0	204	4	US-09-107-279-3240	Sequence 3240, Ap
1150	60.5	5.1	240	2	US-08-114-555A-6	Sequence 6, Appl1	1223	60	5.0	206	3	US-08-513-974B-27	Sequence 27, Appl1
1151	60.5	5.1	240	3	US-08-559-397A-12	Sequence 12, Appl1	1224	60	5.0	206	3	US-08-776-971-122	Sequence 22, Appl1
1152	60.5	5.1	269	4	US-09-248-796A-2276	Sequence 2276, A	1225	60	5.0	206	4	US-09-461-436B-27	Sequence 22, Appl1
1153	60.5	5.1	280	3	US-08-652-877-6	Sequence 6, Appl1	1226	60	5.0	206	4	US-09-576-290-102	Sequence 22, Appl1
1154	60.5	5.1	280	3	US-08-476-515A-6	Sequence 6, Appl1	1227	60	5.0	214	4	US-09-489-039A-11059	Sequence 11059, A
1155	60.5	5.1	283	1	US-08-118-270-78	Sequence 78, Appl1	1228	60	5.0	223	3	US-08-513-974B-315	Sequence 315, App
1156	60.5	5.1	283	5	PCT-US93-08528-78	Sequence 78, Appl1	1229	60	5.0	223	3	US-08-513-974B-364	Sequence 364, App
1157	60.5	5.1	285	4	US-10-162-012-37	Sequence 37, Appl1	1230	60	5.0	223	3	US-08-513-974B-368	Sequence 368, App
1158	60.5	5.1	296	4	US-09-540-236-2856	Sequence 2856, Ap	1231	60	5.0	223	3	US-08-776-971-100	Sequence 100, App
1159	60.5	5.1	300	4	US-09-393-634-17	Sequence 17, Appl1	1232	60	5.0	223	3	US-08-776-971-102	Sequence 102, App
1160	60.5	5.1	342	2	US-08-742-011-2	Sequence 2, Appl1	1233	60	5.0	223	3	US-08-776-971-108	Sequence 108, App
1161	60.5	5.1	342	3	US-09-275-384B-5	Sequence 5, Appl1	1234	60	5.0	223	4	US-09-576-290-100	Sequence 100, App
1162	60.5	5.1	342	3	US-09-116-498-2	Sequence 2, Appl1	1235	60	5.0	223	4	US-09-576-290-102	Sequence 102, App
1163	60.5	5.1	342	3	US-09-449-437A-2	Sequence 9, Appl1	1236	60	5.0	223	4	US-09-576-290-102	Sequence 108, App
1164	60.5	5.1	342	3	US-09-517-605-9	Sequence 9, Appl1	1237	60	5.0	242	3	US-09-576-290-108	Sequence 2, Appl1
1165	60.5	5.1	342	4	US-09-852-156-2	Sequence 2, Appl1	1238	60	5.0	257	4	US-09-543-681A-6362	Sequence 6362, Ap
1166	60.5	5.1	342	4	US-09-721-341-9	Sequence 9, Appl1	1239	60	5.0	273	4	US-09-248-796A-14625	Sequence 14625, A
1167	60.5	5.1	342	4	US-09-721-495B-9	Sequence 9, Appl1	1240	60	5.0	282	4	US-09-270-767-35685	Sequence 35685, A
1168	60.5	5.1	349	4	US-09-710-879-932	Sequence 932, App	1241	60	5.0	282	4	US-09-270-767-35685	Sequence 50907, A
1169	60.5	5.1	352	4	US-09-489-039A-9155	Sequence 9155, Ap	1242	60	5.0	284	4	US-09-270-767-50902	Sequence 26771, A
1170	60.5	5.1	357	4	US-09-107-532A-5132	Sequence 5132, Ap	1243	60	5.0	295	3	US-09-422-968-10	Sequence 10, Appl1
1171	60.5	5.1	359	2	US-08-748-485-5	Sequence 5, Appl1	1244	60	5.0	295	3	US-09-422-968-10	Sequence 10, Appl1
1172	60.5	5.1	388	4	US-09-252-991A-22979	Sequence 22979, A	1245	60	5.0	295	4	US-09-708-015A-10	Sequence 10, Appl1
1173	60.5	5.1	397	4	US-09-107-532A-4918	Sequence 4918, Ap	1246	60	5.0	313	4	US-09-270-767-58683	Sequence 58683, A
1174	60.5	5.1	409	2	US-08-743-130A-2	Sequence 2, Appl1	1247	60	5.0	317	3	US-08-605-284B-17	Sequence 17, Appl1
1175	60.5	5.1	409	2	US-08-743-130A-39	Sequence 39, Appl1	1248	60	5.0	324	4	US-09-543-681A-6241	Sequence 6241, Ap
1176	60.5	5.1	417	4	US-09-248-796A-16410	Sequence 16410, A	1249	60	5.0	326	4	US-09-540-236-3340	Sequence 3340, Ap
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1178	60.5	5.1	446	4	US-09-489-039A-9587	Sequence 9587, Ap	1251	60	5.0	330	4	US-09-543-681A-7116	Sequence 7116, Ap
1179	60.5	5.1	451	4	US-09-328-352-5044	Sequence 5044, Ap	1252	60	5.0	333	4	US-09-170-496B-8	Sequence 8, Appl1
1180	60.5	5.1	473	4	US-09-489-039A-14199	Sequence 14199, A	1253	60	5.0	333	4	US-09-170-496B-168	Sequence 168, App
1181	60.5	5.1	475	4	US-09-270-767-43475	Sequence 43475, A	1254	60	5.0	333	4	US-09-826-509-509	Sequence 509, App
1182	60.5	5.1	487	3	US-09-724-224-8	Sequence 8, Appl1	1255	60	5.0	341	4	US-09-302-540-11473	Sequence 11473, A
1183	60.5	5.1	487	3	US-10-093-317-8	Sequence 8, Appl1	1256	60	5.0	347	4	US-09-107-532A-6019	Sequence 6019, Ap
1184	60.5	5.1	489	4	US-09-986-536-2	Sequence 2, Appl1	1257	60	5.0	359	4	US-09-107-532A-6455	Sequence 6455, Ap
1185	60.5	5.1	490	4	US-09-248-796A-19910	Sequence 19910, A	1258	60	5.0	360	4	US-09-270-767-32827	Sequence 32827, Ap
1186	60.5	5.1	490	4	US-09-949-016-8784	Sequence 8784, Ap	1259	60	5.0	360	4	US-09-270-767-48044	Sequence 48044, A
1187	60.5	5.1	498	4	US-09-107-532A-5082	Sequence 5082, Ap	1260	60	5.0	376	4	US-09-107-532A-6448	Sequence 6448, Ap
1188	60.5	5.1	498	4	US-09-583-110-2949	Sequence 2949, Ap	1261	60	5.0	377	3	US-09-316-080-5	Sequence 5, Appl1
1189	60.5	5.1	499	4	US-09-710-879-1558	Sequence 1558, Ap	1262	60	5.0	382	2	US-09-134-001C-4483	Sequence 4483, Ap
1190	60.5	5.1	503	3	US-09-068-195-24	Sequence 24, Appl1	1263	60	5.0	387	2	US-08-990-379-8	Sequence 6, Appl1
1191	60.5	5.1	510	3	US-09-107-433-2618	Sequence 2618, Ap	1264	60	5.0	397	2	US-08-990-379-8	Sequence 8, Appl1
1192	60.5	5.1	512	3	US-09-724-224-4	Sequence 4, Appl1	1265	60	5.0	416	4	US-09-583-110-2732	Sequence 2732, Ap
1193	60.5	5.1	512	4	US-10-093-317-4	Sequence 4, Appl1	1266	60	5.0	416	4	US-10-140-372-4	Sequence 4, Appl1
1194	60.5	5.1	519	4	US-09-248-796A-20852	Sequence 20852, A	1267	60	5.0	418	4	US-09-107-433-3218	Sequence 3218, Ap
1195	60.5	5.1	533	4	US-09-489-039A-7452	Sequence 7452, Ap	1268	60	5.0	419	1	US-08-385-186-2	Sequence 2, Appl1

1269	60	5.0	419	1	US-08-365-186-4	Sequence 4, Appl1	1342	59.5	5.0	209	4	US-09-813-4538-21	Sequence 21, Appl1
1270	60	5.0	419	4	US-09-270-767-43338	Sequence 43338, A	1343	59.5	5.0	220	4	US-09-107-5328-6603	Sequence 6803, Ap
1271	60	5.0	419	4	US-09-949-016-6002	Sequence 6002, Ap	1344	59.5	5.0	222	4	US-09-107-5328-6747	Sequence 6747, Ap
1272	60	5.0	430	4	US-09-799-978-42	Sequence 42, Appl1	1345	59.5	5.0	249	4	US-09-328-352-4690	Sequence 4690, Ap
1273	60	5.0	421	4	US-09-543-681A-7791	Sequence 7791, Ap	1346	59.5	5.0	268	4	US-09-902-540-14104	Sequence 14104, A
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1275	60	5.0	440	4	US-09-949-016-10558	Sequence 10558, A	1348	59.5	5.0	280	4	US-09-543-681A-6175	Sequence 6175, Ap
1276	60	5.0	448	3	US-09-949-016-10586	Sequence 10586, A	1349	59.5	5.0	281	4	US-09-134-000C-4344	Sequence 4344, Ap
1277	60	5.0	467	3	US-08-867-611-28	Sequence 28, Appl1	1350	59.5	5.0	283	4	US-09-107-5328-4206	Sequence 4206, Ap
1278	60	5.0	467	4	US-09-690-359-28	Sequence 33, Appl1	1351	59.5	5.0	295	4	US-09-543-681A-5660	Sequence 5660, Ap
1279	60	5.0	467	5	PCT-US97-06565A-33	Sequence 33, Appl1	1352	59.5	5.0	324	4	US-09-902-540-12246	Sequence 12246, A
1280	60	5.0	502	1	US-08-484-840-3	Sequence 3, Appl1	1353	59.5	5.0	327	2	US-08-926-724-3	Sequence 3, Appl1
1281	60	5.0	502	1	US-08-483-094-3	Sequence 3, Appl1	1354	59.5	5.0	327	3	US-08-904-032-3	Sequence 3, Appl1
1282	60	5.0	509	4	US-09-134-000C-5949	Sequence 5949, Ap	1355	59.5	5.0	337	4	US-09-540-236-2590	Sequence 2590, Ap
1283	60	5.0	521	4	US-09-538-092-1330	Sequence 1330, Ap	1356	59.5	5.0	341	1	US-08-423-564-5	Sequence 5, Appl1
1284	60	5.0	521	4	US-09-949-016-6672	Sequence 6672, Ap	1357	59.5	5.0	350	1	US-08-118-270-41	Sequence 41, Appl1
1285	60	5.0	521	5	PCT-US93-08386-10	Sequence 10, Appl1	1358	59.5	5.0	350	4	US-09-910-695-8	Sequence 8, Appl1
1286	60	5.0	526	4	US-09-949-016-11505	Sequence 11505, A	1359	59.5	5.0	360	5	PCT-US93-08528-41	Sequence 41, Appl1
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1288	60	5.0	587	4	US-09-538-092-1130	Sequence 1130, Ap	1361	59.5	5.0	370	3	US-09-134-001C-4166	Sequence 4166, Ap
1289	60	5.0	590	3	US-08-893-852A-4	Sequence 4, Appl1	1362	59.5	5.0	388	4	US-09-222-938A-37	Sequence 37, Appl1
1290	60	5.0	590	4	US-08-821-818-2	Sequence 2, Appl1	1363	59.5	5.0	398	4	US-09-583-110-2855	Sequence 2855, Ap
1291	60	5.0	590	4	US-09-052-753B-2	Sequence 2, Appl1	1364	59.5	5.0	399	4	US-09-107-433-3898	Sequence 3898, Ap
1292	60	5.0	626	1	US-07-938-782A-2	Sequence 2, Appl1	1365	59.5	5.0	431	2	US-08-933-750C-24	Sequence 24, Appl1
1293	60	5.0	626	1	US-08-630-524-2	Sequence 2, Appl1	1366	59.5	5.0	431	3	US-09-234-613-24	Sequence 24, Appl1
1294	60	5.0	626	4	US-09-578-441-5	Sequence 5, Appl1	1367	59.5	5.0	439	2	US-08-853-659A-37	Sequence 37, Appl1
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1296	60	5.0	630	4	US-09-602-787A-548	Sequence 548, Ap	1369	59.5	5.0	445	4	US-09-710-279-2644	Sequence 2644, Ap
1297	60	5.0	639	3	US-09-134-001C-5661	Sequence 5661, Ap	1370	59.5	5.0	447	4	US-09-694-519-9	Sequence 9, Appl1
1298	60	5.0	667	2	US-08-718-661-2	Sequence 2, Appl1	1371	59.5	5.0	461	4	US-09-543-681A-4195	Sequence 4195, Ap
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1305	60	5.0	797	4	US-09-949-016-6657	Sequence 6657, Ap	1378	59.5	5.0	738	4	US-09-328-352-4315	Sequence 4315, Ap
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1309	60	5.0	1179	4	US-09-949-016-10545	Sequence 10545, A	1382	59.5	5.0	852	4	US-09-540-236-2304	Sequence 2304, Ap
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1316	60	5.0	1447	4	US-09-724-531-19	Sequence 19, Appl1	1389	59.5	5.0	1469	4	US-09-262-537-58	Sequence 58, Appl1
1317	60	5.0	1447	4	US-08-954-701A-19	Sequence 19, Appl1	1390	59.5	5.0	1471	4	US-08-811-519-1	Sequence 1, Appl1
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1321	60	5.0	2273	4	US-09-032-438C-3	Sequence 3, Appl1	1394	59.5	5.0	2396	4	US-08-747-863-2	Sequence 2, Appl1
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1463	59	4.9	506	4	US-09-719-919A-1	Sequence 1, Appl1
1464	59	4.9	507	4	US-09-949-016-9860	Sequence 9860, Ap
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1467	59	4.9	517	4	US-09-855-323-15	Sequence 15, Appl
1468	59	4.9	578	4	US-09-252-991A-18288	Sequence 18288, A
1469	59	4.9	586	4	US-09-107-532A-6918	Sequence 6918, Ap
1470	59	4.9	586	4	US-09-438-185A-365	Sequence 365, Ap
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1472	59	4.9	581	2	US-08-628-145-10	Sequence 10, Appl
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1484	59	4.9	674	1	US-08-803-872-7	Sequence 7, Appl1
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1486	59	4.9	707	1	US-08-803-973-12	Sequence 12, Appl
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1488	59	4.9	714	2	US-08-990-114-3	Sequence 3, Appl1
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1498	59	4.9	936	4	US-09-252-991A-30190	Sequence 30190, A
1499	59	4.9	1036	4	US-09-252-991A-27075	Sequence 27075, A
1500	59	4.9	1048	4	US-09-949-016-6192	Sequence 6192, Ap

ALIGNMENTS

RESULT 1
US-08-691-814B-6
Sequence 6, Application US/08691814B
Patent No. 5981218
GENERAL INFORMATION:
APPLICANT: Rio, Marie-Christine
APPLICANT: Tomasetto, Catherine
APPLICANT: Bassett, Paul
APPLICANT: Byrne, Jennifer
TITLE OF INVENTION: Isolated Nucleic Acid Molecules Useful
TITLE OF INVENTION: as Leukemia Markers and in Breast Cancer Prognosis
NUMBER OF SEQUENCES: 124
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sterne, Kesseler, Goldstein & Fox P.L.L.C.
STREET: 1100 New York Ave, NW, Suite 600
CITY: Washington
STATE: DC
COUNTRY: USA
ZIP: 20005-3934
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/691,814B
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/002,183
FILING DATE: 09-AUG-1995
ATTORNEY/AGENT INFORMATION:
NAME: Steffe, Eric K.
REGISTRATION NUMBER: 36,688
REFERENCE/DOCKET NUMBER: 1383,0090001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202-371-2600
FAX: 202-371-2543
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 445 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-691-814B-6

Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. 7.5e-68;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

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Qy 112 ILAYAVCRRLRHMAIALTTAVTSAPFLAKVILSKLFSQAGFYVLPPIISFLIAMIETWFL 171
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RESULT 2
US-09-949-016-8594
; Sequence 8594, Application US/09949016
; Patent No. 6812339
; GENERAL INFORMATION:
; APPLICANT: VENTER, J. Craig et al.
; TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED
; TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001307
; CURRENT APPLICATION NUMBER: US/09/949,016
; CURRENT FILING DATE: 2000-04-14
; PRIOR APPLICATION NUMBER: 60/241,755
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 60/237,768
; PRIOR FILING DATE: 2000-10-03
; PRIOR APPLICATION NUMBER: 60/231,498
; PRIOR FILING DATE: 2000-09-08
; NUMBER OF SEQ ID NOS: 207012
; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 8594
; LENGTH: 449
; TYPE: PRT
; ORGANISM: Human
US-09-949-016-8594

Query Match
Best Local Similarity 7.2%; Score 85.5; DB 4; Length 449;
Best Local Similarity 25.5%; Pred. No. 0.41;
Matches 38; Conservative 18; Mismatches 46; Indels 47; Gaps 8;
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Qy 109 KVLILAVAVCRRLRHMAIALTTAVTSAPFLAKVILSKLFSQAGFYVLPPIISFLIAMIETWFL 163
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RESULT 3
US-08-846-762-92
; Sequence 92, Application US/08846762A
; Patent No. 5994072
; GENERAL INFORMATION:
; APPLICANT: Lam, Joseph S.
; APPLICANT: Burrows, Lori
; APPLICANT: Charter, Deborah
; APPLICANT: de Kielevit, Teresa
; TITLE OF INVENTION: No. 5994072e1 Proteins Involved in the Synthesis and Assembly
; TITLE OF INVENTION: of O-Antigen in Pseudomonas Aeruginosa
; FILE REFERENCE: 6580-089
; CURRENT APPLICATION NUMBER: US/08/846,762A
; CURRENT FILING DATE: 1997-04-30
; NUMBER OF SEQ ID NOS: 100
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 92
; LENGTH: 341
; TYPE: PRT

ORGANISM: Pseudomonas aeruginosa
US-08-846-762-92
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Best Local Similarity 6.9%; Score 82.5; DB 2; Length 341;
Best Local Similarity 24.0%; Pred. No. 0.62;
Matches 31; Conservative 20; Mismatches 51; Indels 27; Gaps 4;
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Qy 107 REVVLILAVAVCRRLRHMAIALTTAVTSAPFLAKVILSKLFSQAGFYVLPPIISFLIAMIETWFL 166
Db 283 RFR-----RHLPTVLSAIAINIITWLPFIALAGL-----NIVNPITALLIISYI 325
Qy 167 ETWFLDFKV 175
Db 326 PLIYIDYKL 334

RESULT 4
US-09-489-039A-9711
; Sequence 9711, Application US/09489039A
; Patent No. 6610836
; GENERAL INFORMATION:
; APPLICANT: Gary Breton et. al
; TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
; TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
; FILE REFERENCE: 2709.2004001
; CURRENT APPLICATION NUMBER: US/09/489,039A
; CURRENT FILING DATE: 2000-01-27
; PRIOR APPLICATION NUMBER: US 60/117,747
; PRIOR FILING DATE: 1999-01-29
; NUMBER OF SEQ ID NOS: 14342
; SEQ ID NO 9711
; LENGTH: 350
; TYPE: PRT
; ORGANISM: Klebsiella pneumoniae
US-09-489-039A-9711

Query Match
Best Local Similarity 6.7%; Score 80.5; DB 4; Length 350;
Best Local Similarity 31.8%; Pred. No. 1.1;
Matches 21; Conservative 15; Mismatches 21; Indels 9; Gaps 3;
Qy 111 ILIAYAVCRRLRHMAIALTTAVTSAPFLAKVILSKL-----FSQAGFYVLPPIISFLIAMIETWFL 163
Db 83 LILAVSIPPLAPWMMVVLGTAFA--AVVIAKQVLGGVGHNPFPNAMIQYVVLISFPVQMT 140
Qy 164 AMLETW 169
Db 141 SWLPSY 146

RESULT 5
US-09-171-699-4
; Sequence 4, Application US/09171699
; Patent No. 6448389
; GENERAL INFORMATION:
; APPLICANT: The Wistar Institute of, Anatomy & Biology
; APPLICANT: Gonczol, Eva
; APPLICANT: Berencsi, Klara
; TITLE OF INVENTION: No. 6448389e1 Cytomegalovirus DNA Constructs and
; TITLE OF INVENTION: Uses Therefor
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Howson and Howson
; STREET: Spring House Corporate Center, P.O. Box 457
; CITY: Spring House
; STATE: Pennsylvania
; COUNTRY: USA
; ZIP: 19477
; COMPUTER READABLE FORM:

[illegible]

```

Query Match      6.7% ; Score 79.5; DB 5; length 406;
Best Local Similarity 19.3% ; Pred. No. 1.8;
Matches 52; Conservative 36; Mismatches 67; Indels 115; Gaps 12;

QY      14 GSOSHSALNINHSINPTQMARIESY-----EGERKKGISDVARTCLFVTFDLFPVTL 68
      142 GCSGMAALATNLPGCSPDEIMAYAKFKFLIDBERDK-----VLTHIDHIFNDI 190
QY      69 LWTIELNVNGIENTLEKEVWQYDY-----YSSYFDIFLLAVPRFKVLLIYAVCRL 120
      191 L-----TTCVETMCNEKYVTSDCAMWTWGGISLSEF-----CRV 226
Db

QY      121 RHMWALTLTVAVTSAPFLAK-----VLISKLFSGCAFQYVL----- 156
      227 LSCVLEETSV-----MLAKRPLITKEVISVMKRRIEIECMKFAQ-----YIIGADPLR 277
Db

QY      157 ---PIISFILAMIEFWFLDKVLPQEAEEFENRLLIVDASERALLIPGSLSDGFQFSPPE 213
      278 VCSPSVD-----DLRAIAEESDEEBATAYVLTATL-----GASSSDSLVSPPE 320
Db

QY      214 S-----EAGSEEAEEKQOSEK 229
      321 SPVPATTPPLSSVIVAENSDOEESQSEEE 350
Db

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Query Match	6.7%	Score	79.5	DB	4	Length	723
Best Local Similarity	18.0%	Pred. No.	4				
Matches	34	Conservative	40	Mismatches	58	Indels	57
						Gaps	8

SEQ ID NO 14
LENGTH: 766
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-653-14

Query Match
Best Local Similarity 18.0%; Pred. No. 5.7; Length 766;
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTPLDILFVTLMIIEINLVNGIENLEKEVMQDYSSYFDIFLLAVRFFKVL-----GAFGY 154
DB 13 FMSVDICVTIAIVF-----SHLDRSLIEDIRHFNIPDSVLDIWAACLYRSCLLGATIG 67
QY 113 ----LAVAVCRRL-HMMALITTAIVTSAPFLAVIISKLSQ-----GAFGY 154
DB 68 VAKNSALGPRRLASMLVITLVCLEFGIYAMVKLL--LPESEVRPRIRDPWFALFWMTY 124
QY 155 VLPIISFILAMIEFWFLDFKVLPOEABEENRLLIVODASERALLIPGSLSDGQFY----- 209
DB 125 ISLGASFLMLWL-----LSTVRGCTQ--ALPEGAITEAGFPQSGR 163
QY 210 SPPESEAGS 218
DB 164 PPPEQASGA 172

RESULT 12
US-09-724-653-15
Sequence 15, Application US/09724653
Patent No. 6830913
GENERAL INFORMATION:
APPLICANT: Ling, Victor
TITLE OF INVENTION: NOVEL ABCB9 TRANSPORTER AND USES THEREOF
FILE REFERENCE: APZ-004CP
CURRENT APPLICATION NUMBER: US/09/724,653
CURRENT FILING DATE: 2000-11-28
PRIOR APPLICATION NUMBER: 60/167,930
PRIOR FILING DATE: 1999-11-29
NUMBER OF SEQ ID NOS: 20
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 15
LENGTH: 766
TYPE: PRT
ORGANISM: Homo sapiens
US-09-724-653-15

Query Match
Best Local Similarity 18.0%; Pred. No. 5.7; Length 766;
Matches 34; Conservative 39; Mismatches 59; Indels 57; Gaps 8;

QY 58 FVTPLDILFVTLMIIEINLVNGIENLEKEVMQDYSSYFDIFLLAVRFFKVL----- 112
DB 13 FMSVDICVTIAIVF-----SHLDRSLIEDIRHFNIPDSVLDIWAACLYRSCLLGATIG 67
QY 113 ----LAVAVCRRL-HMMALITTAIVTSAPFLAVIISKLSQ-----GAFGY 154
DB 68 VAKNSALGPRRLASMLVITLVCLEFGIYAMVKLL--LPESEVRPRIRDPWFALFWMTY 124
QY 155 VLPIISFILAMIEFWFLDFKVLPOEABEENRLLIVODASERALLIPGSLSDGQFY----- 209
DB 125 ISLGASFLMLWL-----LSTVRGCTQ--ALPEGAITEAGFPQSGR 163
QY 210 SPPESEAGS 218
DB 164 PPPEQASGA 172

RESULT 13
US-09-248-796A-20444
Sequence 20444, Application US/09248796A
Patent No. 6747137
GENERAL INFORMATION:

APPLICANT: Keith Weinstein et al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO CANDIDA ALBICANS
TITLE OF INVENTION: FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.132
CURRENT APPLICATION NUMBER: US/09/248,796A
CURRENT FILING DATE: 1999-02-12
PRIOR APPLICATION NUMBER: US 60/074,725
PRIOR FILING DATE: 1998-02-13
PRIOR APPLICATION NUMBER: US 60/096,409
PRIOR FILING DATE: 1998-08-13
NUMBER OF SEQ ID NOS: 28208
SEQ ID NO 20444
LENGTH: 228
TYPE: PRT
ORGANISM: Candida albicans
US-09-248-796A-20444

Query Match
Best Local Similarity 22.1%; Pred. No. 1.2; Length 228;
Matches 32; Conservative 32; Mismatches 49; Indels 32; Gaps 7;

QY 63 LRFVTL-----LMIIEINLVNGIENLEKEVMQDYSSYFDIFLLAVRFFKVL----- 106
DB 91 LVFTALTSGAFWLSFPAINIPFGILAAQKMDTSLASALAFYLAMALISPIFMLTF 150
QY 107 RFRVTLIAYAVCRRLHMMALITTAIVTSAPFLAVIISKLSQSGAFGYVLPISF----- 161
DB 151 KSTVLSGFFLC-----LTALPSLSASIFVGSVALTK--MAGARVIAVVALYDTFA 202
QY 162 ILAMIEFWFLDFKVLPOEABE 183
DB 203 LATKQNSYFTLPVILPGEAKQE 227

RESULT 14
US-09-270-767-43373
Sequence 43373, Application US/09270767
Patent No. 6703491
GENERAL INFORMATION:
APPLICANT: Homburger et al.
TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
FILE REFERENCE: File Reference: 7326-094
CURRENT APPLICATION NUMBER: US/09/270,767
CURRENT FILING DATE: 1999-03-17
NUMBER OF SEQ ID NOS: 62517
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 43373
LENGTH: 251
TYPE: PRT
ORGANISM: Drosophila melanogaster
US-09-270-767-43373

Query Match
Best Local Similarity 18.8%; Pred. No. 1.3; Length 251;
Matches 34; Conservative 46; Mismatches 63; Indels 38; Gaps 6;

QY 5 PEDMENAL--TSGQSSHASIRNHSINPTQMARISYBERREKGSIDVARTCLPTFD 62
DB 51 PDSADNAVIESGIQSNLDVQGDIN--RPTDLSLAE--KKKDAADRKTGTFTDAP 103
QY 63 LRFVTLMIIEINLVNGIENLEKEVMQDYSSYFDIFLLAVRFFKVLILAVAVCRRLH 122
DB 104 TASISVILTELG-----DITFPIAMAMRHRLIYFGAIA----- 141
QY 123 WMAIALTTAVTSAPFLAVIISKLSQSGAFGYVLPISFILAMIEFWFLDFKVLPOEABE 182
DB 142 --ALAMTILISCAFGMAANFIPKIYT-----YISTALFLIPGLKMLYDGYKMKPTDAQE 194
QY 183 E 183
DB 195 E 195

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OM protein - protein search, using sw model

Run on: May 17, 2005, 10:16:30 ; Search time 63 Seconds
(without alignments)
1902.008 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNTLPEMDNALTGSSQSHA.....EAGSEAEKQDSKPLLEL 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues
Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Listing first 1500 summaries

Database : Uniprot 03:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1195	100.0	234	1 MENT_HUMAN	Q95772 homo sapien
2	1134.5	94.9	235	1 MENT_MOUSE	Q95413 mus musculu
3	796	66.6	227	2 Q6DI38	Q6DI38 brachydanio
4	700.5	58.6	227	2 Q6DER7	Q6DER7 xenopus tro
5	698.5	58.5	444	2 Q6PFA0	Q6PFA0 xenopus lae
6	684	57.2	448	2 Q6GNT3	Q6GNT3 xenopus lae
7	664	55.6	445	1 ML64_HUMAN	Q14849 homo sapien
8	656.5	54.9	446	1 ML64_MOUSE	Q61542 mus musculu
9	632	52.9	448	2 Q6PH03	Q6PH03 brachydanio
10	492	41.2	107	2 Q8BWP8	Q8BWP8 m mus muscu
11	348	29.1	568	2 Q7QIR3	Q7QIR3 anopheles g
12	343	28.7	545	2 Q8MZH4	Q8MZH4 drosophila
13	343	28.7	583	2 Q9W145	Q9W145 drosophila
14	204	17.1	447	2 Q19819	Q19819 caenorhabdi
15	104.5	8.7	294	1 ML64_SALPO	Q90289 salvelinus
16	102.5	8.6	348	2 Q97Y00	Q97Y00 eulitobus
17	93.5	7.8	424	2 Q9UZW1	Q9UZW1 pyrococcus
18	93.5	7.8	564	2 Q8HQ10	Q8HQ10 thirids imag
19	91	7.6	246	2 Q8DU10	Q8DU10 streptococc
20	91	7.6	525	2 Q7VPT4	Q7VPT4 helicobacte
21	91	7.6	651	2 Q8DZK0	Q8DZK0 streptococc
22	91	7.6	651	2 Q8ESW0	Q8ESW0 streptococc
23	90.5	7.6	262	2 Q7NBJ4	Q7NBJ4 mycoplasma
24	90	7.5	1911	2 Q02038	Q02038 cyanea capi
25	89.5	7.5	233	2 Q6JCT3	Q6JCT3 aleurodicus
26	89.5	7.5	367	2 Q8HEH8	Q8HEH8 varroa dest
27	89.5	7.5	376	2 Q6JCT6	Q6JCT6 aleurodicus
28	89.5	7.5	488	2 Q840W7	Q840W7 streptococc
29	89	7.4	384	2 Q7RTB5	Q7RTB5 plasmodium
30	88.5	7.4	384	2 Q6MNV4	Q6MNV4 iana catesb
31	87	7.3	304	2 Q640E5	Q640E5 xenopus lae

32	87	7.3	610	2 Q7RRS2	Q7RRS2 plasmodium
33	87	7.3	707	2 Q6GN42	Q6GN42 xenopus lae
34	86.5	7.2	720	2 Q8PYM2	Q8PYM2 methanocarc
35	86.5	7.2	328	2 Q7NLL9	Q7NLL9 gloebacter
36	86.5	7.2	605	2 Q7Z205	Q7Z205 caenorhabdi
37	86.5	7.2	891	2 Q8UJA2	Q8UJA2 ectromella
38	86	7.2	1050	2 Q871G6	Q871G6 neurospora
39	86	7.2	1056	2 Q7S7L6	Q7S7L6 neurospora
40	85.5	7.2	174	2 P97067	P97067 salmonella
41	85.5	7.2	336	2 Q95086	Q95086 homo sapien
42	85.5	7.2	339	2 Q95089	Q95089 homo sapien
43	85.5	7.2	336	2 Q9PME5	Q9PME5 campylobact
44	85.5	7.2	438	1 CLN3_HUMAN	CLN3266 homo sapien
45	85.5	7.2	473	1 PSS1_HUMAN	P48651 streptomyce
46	85.5	7.2	747	1 Q93GL8	Q93GL8 salmonella
47	85	7.1	348	2 Q9SFI7	Q9SFI7 arabidopsis
48	85	7.1	377	2 Q612C1	Q612C1 bacillus an
49	85	7.1	448	2 Q51531	Q51531 borrelia bu
50	85	7.1	797	2 Q82GJ8	Q82GJ8 streptomyce
51	84.5	7.1	471	1 PSS1_MOUSE	Q99182 mus musculu
52	84.5	7.1	473	1 Q6A0E5	Q6A0E5 mus musculu
53	84.5	7.1	467	2 Q6A0E5	Q6A0E5 mus musculu
54	84.5	7.1	892	2 Q9JF90	Q9JF90 vaccinia vi
55	84.5	7.1	1118	2 Q65U88	Q65U88 manheimela
56	84	7.0	469	2 Q9HJK8	Q9HJK8 thermoplasma
57	84	7.0	493	2 Q7TSJ7	Q7TSJ7 mus musculu
58	84	7.0	1700	2 Q75JN1	Q75JN1 dicystosrell
59	83.5	7.0	275	2 Q8XIT3	Q8XIT3 clostridium
60	83.5	7.0	303	2 Q6FNB8	Q6FNB8 candida gla
61	83.5	7.0	332	2 Q8LB40	Q8LB40 arabidopsis
62	83.5	7.0	352	2 Q97K11	Q97K11 clostridium
63	83.5	7.0	355	2 Q6K124	Q6K124 mycoplasma
64	83.5	7.0	380	2 Q97C55	Q97C55 thermoplasma
65	83.5	7.0	450	2 Q9CTA9	Q9CTA9 mus musculu
66	83.5	7.0	559	2 Q6PCX2	Q6PCX2 mus musculu
67	83.5	7.0	662	2 Q8BP20	Q8BP20 pseudomonas
68	83.5	7.0	834	2 Q9JHF5	Q9JHF5 mus musculu
69	83.5	7.0	834	2 Q9JL12	Q9JL12 mus musculu
70	83.5	7.0	834	2 Q91W06	Q91W06 mus musculu
71	83.5	7.0	1034	2 Q7Z2B9	Q7Z2B9 trypanosoma
72	83	6.9	238	2 Q6YR96	Q6YR96 onion yello
73	83	6.9	248	2 Q8GCS6	Q8GCS6 eubacterium
74	83	6.9	291	2 Q8ZDT0	Q8ZDT0 yersinia pe
75	83	6.9	589	2 Q7TWM1	Q7TWM1 mus musculu
76	83	6.9	580	2 Q84192	Q84192 critidia o
77	83	6.9	1056	2 Q8C2V1	Q8C2V1 mus musculu
78	83	6.9	2661	2 Q7RMS4	Q7RMS4 plasmodium
79	82.5	6.9	174	2 P97231	P97231 salmonella
80	82.5	6.9	186	1 TRS2_ECOLI	P14458 escherichia
81	82.5	6.9	186	2 Q7BBW2	Q7BBW2 salmonella
82	82.5	6.9	239	1 Y247_MYCGE	P47489 mycoplasma
83	82.5	6.9	341	2 Q56918	Q56918 yersinia en
84	82.5	6.9	367	2 Q8HCK3	Q8HCK3 varroa dest
85	82.5	6.9	406	2 Q8H749	Q8H749 lactococcus
86	82.5	6.9	419	2 Q19134	Q19134 oryctolagus
87	82.5	6.9	471	2 Q9QW77	Q9QW77 cricetus
88	82.5	6.9	510	2 Q950M6	Q950M6 rhizophyidi
89	82.5	6.9	604	2 Q8RH03	Q8RH03 fusobacteri
90	82.5	6.9	717	1 TRD1_ECOLI	Q87133 escherichia
91	82.5	6.9	717	2 Q87742	Q87742 escherichia
92	82.5	6.9	891	2 Q57223	Q57223 vaccinia vi
93	82.5	6.9	891	2 Q6J3A9	Q6J3A9 vaccinia vi
94	82.5	6.9	891	2 Q80DW2	Q80DW2 campox viru
95	82.5	6.9	892	2 Q6RZH3	Q6RZH3 rabbitpox v
96	82.5	6.9	894	2 Q8QWU0	Q8QWU0 campox viru
97	82.5	6.9	1022	2 Q88V00	Q88V00 lactobacilli
98	82	6.9	156	2 Q81501	Q81501 hepatitis c
99	82	6.9	161	2 Q69UD2	Q69UD2 oryza sativ
100	82	6.9	303	2 Q8RLZ3	Q8RLZ3 haemophilus
101	82	6.9	303	2 Q8RLZ3	Q8RLZ3 haemophilus
102	82	6.9	461	2 Q6AHH8	Q6AHH8 leishonia x
103	82	6.9	472	2 Q70J50	Q70J50 haemophilus
104	82	6.9	587	2 Q6C0H8	Q6C0H8 yarrowia li

105	82	6.9	589	1	RGPI_MOUSE	P46061	mus musculus	178	80	6.7	300	2	Q9C940	Q9C940	arabidopsis
106	82	6.9	589	2	Q91Y52	Q91Y52	mus musculus	179	80	6.7	309	1	RTM1_YEAST	P40113	saccharomyc
107	82	6.9	589	2	Q8C2R3	Q8C2R3	mus musculus	180	80	6.7	343	1	Q7UB59	Q7UB59	rhodospirill
108	82	6.9	589	2	Q6NZB5	Q6NZB5	mus musculus	181	80	6.7	347	2	Q9PFM1	Q9PFM1	arabidopsis
109	82	6.9	646	2	Q6ZPH4	Q6ZPH4	mus musculus	182	80	6.7	355	2	Q7JJA5	Q7JJA5	treponema d
110	82	6.9	647	2	Q8PXU3	Q8PXU3	methanosaec	183	80	6.7	359	2	Q7NAF8	Q7NAF8	phototrichu
111	82	6.9	989	2	Q6CDB6	Q6CDB6	Yarrowia li	184	80	6.7	360	2	Q9H1X3	Q9H1X3	homo sapien
112	82	6.9	1031	2	Q81564	Q81564	plasmodium	185	80	6.7	388	2	Q58427	Q58427	pyrococcus
113	82	6.9	1466	2	P78576	P78576	emeritella	186	80	6.7	448	2	Q650S8	Q650S8	oryza sativ
114	81.5	6.8	190	2	Q9K1A9	Q9K1A9	escherichia	187	80	6.7	540	2	Q6FXI7	Q6FXI7	candida gla
115	81.5	6.8	297	2	Q9B893	Q9B893	schistosoma	188	80	6.7	650	2	Q699P8	Q699P8	anopheles g
116	81.5	6.8	311	2	Q8CD14	Q8CD14	mus musculus	189	80	6.7	661	2	Q759Y6	Q759Y6	asbyra goss
117	81.5	6.8	349	1	RNFD_PASNU	Q9VC0	candidatus	196	79.5	6.7	391	2	Q6T196	Q6T196	helicobacte
118	81.5	6.8	352	2	Q9H7C5	Q9H7C5	pasteurella	190	80	6.7	680	2	Q7VH08	Q7VH08	helicobacte
119	81.5	6.8	387	2	Q72CJ7	Q72CJ7	desulfovibr	191	80	6.7	700	2	Q720Z1	Q720Z1	listeria mo
120	81.5	6.8	414	2	Q6PAH4	Q6PAH4	mus musculus	192	80	6.7	3010	2	Q9Q1Y9	Q9Q1Y9	listeria mo
121	81.5	6.8	438	2	Q35934	Q35934	mus musculus	193	79.5	6.7	269	2	Q722B0	Q722B0	listeria mo
122	81.5	6.8	438	2	Q8CSB1	Q8CSB1	mus musculus	194	79.5	6.7	307	2	Q89NC2	Q89NC2	bradyrhizob
123	81.5	6.8	447	2	Q7VR0C	Q7VR0C	brachydanio	195	79.5	6.7	367	2	Q8ESY3	Q8ESY3	oceanobacti
124	81.5	6.8	465	2	Q803C9	Q803C9	homo sapien	196	79.5	6.7	438	2	CLN3_CANFA	CLN3_CANFA	xiptinema a
125	81.5	6.8	519	2	Q9NVS8	Q9NVS8	homo sapien	197	79.5	6.7	463	2	Q92E13	Q92E13	canis fami
126	81.5	6.8	577	2	Q6P1Z6	Q6P1Z6	homo sapien	198	79.5	6.7	488	2	Q6OU70	Q6OU70	aspergillus
127	81.5	6.8	577	2	Q7Z748	Q7Z748	homo sapien	200	79.5	6.7	491	1	VIB1_HCMVT	VIB1_HCMVT	human cytom
128	81.5	6.8	645	2	Q6TU09	Q6TU09	oryza sativ	201	79.5	6.7	546	1	FVR2_RAT	FVR2_RAT	rattus norv
129	81.5	6.8	716	2	Q8DLB4	Q8DLB4	synecococc	202	79.5	6.7	558	2	Q51954	Q51954	borrelia be
130	81.5	6.8	735	2	Q6B3Y6	Q6B3Y6	escherichia	203	79.5	6.7	649	2	Q6BZ08	Q6BZ08	debaromyce
131	81.5	6.8	892	2	Q8V2P5	Q8V2P5	camelipox vi	204	79.5	6.7	674	2	Q86P19	Q86P19	drosophila
132	81.5	6.8	892	2	Q75SR6	Q75SR6	camelipox vi	205	79.5	6.7	726	2	Q9EJU3	Q9EJU3	salmonella
133	81.5	6.8	1092	2	Q755K6	Q755K6	asbyra goss	206	79.5	6.7	784	2	Q9VYU0	Q9VYU0	drosophila
134	81.5	6.8	1480	2	Q7R386	Q7R386	giardia lam	207	79.5	6.7	784	2	Q8KDB0	Q8KDB0	chlorobium
135	81	6.8	385	2	Q9Z069	Q9Z069	arabidopsis	208	79.5	6.7	3409	2	Q7S1Z7	Q7S1Z7	neurospora
136	81	6.8	410	2	Q6D043	Q6D043	erwinia car	209	79	6.6	114	2	Q6VRR6	Q6VRR6	helicobacte
137	81	6.8	486	2	Q63E77	Q63E77	baicillus ce	210	79	6.6	251	2	Q6M012	Q6M012	methanococ
138	81	6.8	520	1	Y0U1_CAEEL	P30638	caenorhabdi	211	79	6.6	300	2	Q80ZK3	Q80ZK3	arvicantocis
139	81	6.8	532	1	YHB7_YEAST	P38745	raiscronia s	212	79	6.6	308	2	Q8RGM6	Q8RGM6	fusobacteri
140	81	6.8	805	2	Q8XST5	Q8XST5	hepatocitis c	213	79	6.6	312	2	Q6KH29	Q6KH29	mycoplasma
141	81	6.8	3010	2	Q8QRUL	Q8QRUL	hepatocitis c	214	79	6.6	323	2	Q7KS19	Q7KS19	drosophila
142	80.5	6.7	174	2	P97066	P97066	salmonella	215	79	6.6	349	1	RNFD_BUCCAP	RNFD_BUCCAP	buchnera ap
143	80.5	6.7	242	2	Q8TNE9	Q8TNE9	methanosaec	216	79	6.6	356	2	Q7MG43	Q7MG43	vibrio vuln
144	80.5	6.7	322	2	Q9SNB5	Q9SNB5	arabidopsis	217	79	6.6	375	2	Q887L9	Q887L9	pseudomonas
145	80.5	6.7	353	1	MLIA_PHOSU	P49217	rhodopus su	218	79	6.6	484	2	Q6NIE0	Q6NIE0	corynebacte
146	80.5	6.7	366	2	Q86KX8	Q86KX8	dictyosteli	219	79	6.6	770	2	Q64OD3	Q64OD3	bacteroides
147	80.5	6.7	417	1	Q9SU09	Q9SU09	echinosacch	220	79	6.6	1531	2	Q96195	Q96195	homo sapien
148	80.5	6.7	417	1	TNAB_PROVU	P28785	proteus vul	221	79	6.6	1679	2	Q86TBS	Q86TBS	homo sapien
149	80.5	6.7	463	2	Q8Y988	Q8Y988	listeria mo	222	79	6.6	3010	2	Q9J3H8	Q9J3H8	hepatitis c
150	80.5	6.7	463	2	Q722Q4	Q722Q4	listeria mo	223	79	6.6	3010	2	Q9Q1Z0	Q9Q1Z0	hepatitis c
151	80.5	6.7	486	2	Q9G861	Q9G861	malawimonas	224	78.5	6.6	239	1	Y247_MYCPN	Y247_MYCPN	mycoplasma
152	80.5	6.7	536	1	MYIN_CHLTR	Q46378	chlamydia t	225	78.5	6.6	359	2	Q92DI5	Q92DI5	streptomyce
153	80.5	6.7	548	2	Q7RC45	Q7RC45	plasmodium	226	78.5	6.6	313	2	Q9LOB3	Q9LOB3	streptomyce
154	80.5	6.7	599	2	Q91MB6	Q91MB6	human rotav	227	78.5	6.6	358	1	RNFD_HAEIN	RNFD_HAEIN	haemophilus
155	80.5	6.7	644	1	YNLS_YEAST	P53925	saccharomyc	228	78.5	6.6	380	2	Q8A6F8	Q8A6F8	bacteroides
156	80.5	6.7	644	2	Q6B2V3	Q6B2V3	saccharomyc	229	78.5	6.6	382	2	Q64V54	Q64V54	bacteroides
157	80.5	6.7	732	2	Q6S1Z5	Q6S1Z5	escherichia	230	78.5	6.6	418	2	Q65LP8	Q65LP8	baicillus li
158	80.5	6.7	738	1	TRD2_ECOLI	P22708	escherichia	231	78.5	6.6	451	2	Q65UD5	Q65UD5	manheimia
159	80.5	6.7	738	2	Q7AK62	Q7AK62	plasmid f10	232	78.5	6.6	471	1	SH2A_CRIGR	SH2A_CRIGR	cricketula
160	80.5	6.7	891	1	VP4A_VACCC	Q70462	vaccinia vi	233	78.5	6.6	512	2	Q8G1D7	Q8G1D7	bruceila su
161	80.5	6.7	891	1	VP4A_VACCV	P16715	vaccinia vi	234	78.5	6.6	666	1	KUP_STRAS	KUP_STRAS	streptococc
162	80.5	6.7	891	2	Q8V4W5	Q8V4W5	monkeypox v	235	78.5	6.6	678	2	Q61710	Q61710	mus musculus
163	80.5	6.7	891	2	Q76Z05	Q76Z05	vaccinia vi	236	78.5	6.6	681	2	Q769F3	Q769F3	homo sapien
164	80.5	6.7	1687	2	Q7SC49	Q7SC49	neurospora	237	78.5	6.6	683	2	Q769F4	Q769F4	homo sapien
165	80.5	6.7	1780	2	Q9ZT82	Q9ZT82	arabidopsis	238	78.5	6.6	766	1	ABCS_HUMAN	ABCS_HUMAN	homo sapien
166	80	6.7	156	2	Q9RXJ3	Q9RXJ3	deinococcus	239	78.5	6.6	769	2	Q6P2Q0	Q6P2Q0	homo sapien
167	80	6.7	156	2	Q81513	Q81513	hepatitis c	240	78.5	6.6	6473	2	Q81KH9	Q81KH9	plasmodium
168	80	6.7	238	2	Q9YMX2	Q9YMX2	caenorhabdi	241	78	6.5	188	2	Q81YX2	Q81YX2	baicillus an
169	80	6.7	238	2	Q95KH1	Q95KH1	macaca fasc	242	78	6.5	219	2	Q8W2Y0	Q8W2Y0	oryza sativ
170	80	6.7	255	2	Q6V7H6	Q6V7H6	equine arte	243	78	6.5	226	2	Q7R829	Q7R829	avian infec
171	80	6.7	280	2	Q635R8	Q635R8	baicillus ce	244	78	6.5	240	2	Q9C9P6	Q9C9P6	pasteurella
172	80	6.7	280	2	Q731V3	Q731V3	baicillus ce	245	78	6.5	245	2	P946Z5	P946Z5	clostridium
173	80	6.7	280	2	Q819H0	Q819H0	baicillus ce	246	78	6.5	252	2	Q6B8K2	Q6B8K2	gracilaria
174	80	6.7	280	2	Q81MM0	Q81MM0	baicillus an	247	78	6.5	259	2	Q9KD13	Q9KD13	baicillus ha
175	80	6.7	280	2	Q6HEFS	Q6HEFS	baicillus th	248	78	6.5	331	2	Q96XC4	Q96XC4	sulfolobus
176	80	6.7	290	2	Q99UM2	Q99UM2	staphylococ	249	78	6.5	339	2	Q8D4K9	Q8D4K9	vibrio vuln
177	80	6.7	290	2	Q7A5Y6	Q7A5Y6	staphylococ	250	78	6.5	360	2	Q951A3	Q951A3	tetrahymena

251	78	6.5	382	2	097HC3	097hc3 clostridium	324	77	6.4	650	2	08NTK4	08nuk4 staphylococ
252	78	6.5	414	2	08TN61	08tn61 methanosarc	325	77	6.4	650	2	099Q27	099q27 staphylococ
253	78	6.5	428	2	08DSY9	08dsy9 vibrio vuln	326	77	6.4	650	2	07A374	07a374 staphylococ
254	78	6.5	431	2	09JRS0	09jrs0 actinobacil	327	77	6.4	650	2	08G633	08g633 staphylococ
255	78	6.5	442	2	07MD08	07md08 vibrio vuln	328	77	6.4	650	2	06G633	06g633 staphylococ
256	78	6.5	471	1	Y872 HAEIN	Y872 haemophilus	329	77	6.4	722	2	0632R1	0632r1 bacillus ce
257	78	6.5	486	2	06HMA9	06hma9 bacillus th	330	77	6.4	738	2	08L838	08l838 staphylococ
258	78	6.5	545	2	06FSW9	06fsw9 candida gla	331	77	6.4	789	1	FTSK STAAM	08nw8 staphylococ
259	78	6.5	641	2	09LIC2	09lic2 arabadopsis	332	77	6.4	789	2	06G9T7	06g9t7 staphylococ
260	78	6.5	650	2	07Q6Q8	07q6q8 anapneles g	333	77	6.4	836	2	07Z1F2	07z1f2 plasmodium
261	78	6.5	688	2	098M77	098m77 rhizobium 1	334	77	6.4	877	2	0750H8	0750h8 ashbya goss
262	78	6.5	1297	2	09Y817	09y817 echizosacch	335	77	6.4	991	2	081330	081330 staphylococ
263	78	6.5	2136	1	YCF2 MARPO	YCF2 marphania	336	77	6.4	1024	2	08IKZ6	08ikz6 plasmodium
264	78	6.5	7180	1	R1AB_CWJH	R19751 m repliCase	337	77	6.4	1024	2	07Z1P1	07z1p1 plasmodium
265	77.5	6.5	176	2	0976T7	0976t7 sulfolobus	338	77	6.4	1025	2	025593	025593 plasmodium
266	77.5	6.5	190	2	09K1A8	09k1a8 escherichia	339	77	6.4	1117	2	09M133	09m133 arabadopsis
267	77.5	6.5	263	2	073DX2	073dx2 bacillus ce	340	77	6.4	1477	2	06FTR9	06ftr9 candida gla
268	77.5	6.5	263	2	081I83	081i83 bacillus ce	341	77	6.4	1500	2	092U84	092u84 arabadopsis
269	77.5	6.5	269	2	08Y8T5	08y8t5 listeria mo	342	77	6.4	3010	2	068788	068788 hepatitis c
270	77.5	6.5	270	2	08H1Y1	08h1y1 perognathus	343	77	6.4	3010	2	081757	081757 hepatitis c
271	77.5	6.5	270	2	08H1Y2	08h1y2 perognathus	344	77	6.4	3010	2	09J3G4	09j3g4 hepatitis c
272	77.5	6.5	270	2	08H1Y3	08h1y3 perognathus	345	77	6.4	3013	2	06J6P5	06j6p5 hepatitis c
273	77.5	6.5	294	2	08H1Y4	08h1y4 perognathus	346	77	6.4	4416	2	09J3F3	09j3f3 murine hepa
274	77.5	6.5	294	2	08E130	08e130 oceanobacil	347	77	6.4	4416	2	09J3F8	09j3f8 murine hepa
275	77.5	6.5	299	2	066PT9	066ft9 yersinia ps	348	77	6.4	7124	1	R1AB_CW2	09pya3 m repliCase
276	77.5	6.5	299	2	08ZAL1	08zal1 yersinia ps	349	77	6.4	278	2	08XBFO	08xbfo escherichia
277	77.5	6.5	310	2	08D1I6	08d1i6 yersinia pe	350	76.5	6.4	281	2	08SKS9	08sk9 ancylostoma
278	77.5	6.5	327	2	09PQJ1	09pqj1 ureaplasma	351	76.5	6.4	282	2	092WV5	092wv5 rhizobium m
279	77.5	6.5	328	2	09K6B6	09k6b6 bacillus ha	352	76.5	6.4	342	2	07Z290	07z290 caenorhabdi
280	77.5	6.5	338	2	042882	042882 echizosacch	353	76.5	6.4	352	1	RNPD_SALT1	08z69 salmonella
281	77.5	6.5	365	2	08R770	08r770 thermoaer	354	76.5	6.4	352	1	RNPD_SALT1	08z69 salmonella
282	77.5	6.5	379	2	048008	048008 perognathus	355	76.5	6.4	379	1	CYB_DIPOR	08z69 salmonella
283	77.5	6.5	392	2	08G7P7	08g7p7 bifidobacte	356	76.5	6.4	379	2	09GBY7	09gbw3 dipodomys o
284	77.5	6.5	411	2	09P6V5	09p6v5 echizosacch	357	76.5	6.4	380	2	08HN17	08h17 ochocora pa
285	77.5	6.5	422	2	09HKX6	09hkx6 thermoplasma	358	76.5	6.4	395	2	08KHK2	08kh2 pseudomonas
286	77.5	6.5	440	2	09ZYX3	09zyx3 pedinomonas	359	76.5	6.4	415	2	07UB13	07ub3 shigella fl
287	77.5	6.5	458	2	062XT1	062xt1 bacillus 11	360	76.5	6.4	415	2	083PL5	083pl5 shigella fl
288	77.5	6.5	483	2	09G8V8	09g8v8 rhodomonas	361	76.5	6.4	438	1	CLN3 MOUSE	081124 mus musculus
289	77.5	6.5	491	2	028284	028284 archaeoglob	362	76.5	6.4	439	2	064SNO	064sno bacteroides
290	77.5	6.5	491	2	06SX10	06sx10 human cytom	363	76.5	6.4	451	2	066OT8	066ot8 borrelia ga
291	77.5	6.5	512	2	08YGI2	08ygi2 bruceila me	364	76.5	6.4	452	2	06ZG24	06z24 oryza sativ
292	77.5	6.5	556	2	089180	089180 variola vir	365	76.5	6.4	468	2	082V00	082v00 nltrosomona
293	77.5	6.5	556	2	089232	089232 variola vir	366	76.5	6.4	468	1	YDBM_CABEL	091904 caenorhabdi
294	77.5	6.5	567	2	07RNKO	07rnko plasmodium	367	76.5	6.4	480	2	06SX39	06sx39 human cytom
295	77.5	6.5	620	2	08EKAL	08ekal strewnella	368	76.5	6.4	491	2	06SWP6	06swp6 human cytom
296	77.5	6.5	734	1	NUSC_ORYSA	P12129 oryza sativ	369	76.5	6.4	500	2	06ZTH3	06zth3 sulfolobus
297	77.5	6.5	892	2	VP4A_VARY	P33817 variola vir	370	76.5	6.4	526	1	FVR2_HUMAN	09up33 homo sapien
298	77.5	6.5	892	2	09QNT0	09qnt0 variola min	371	76.5	6.4	538	2	07VP70	07vp70 haemophilus
299	77.5	6.5	979	2	07MLV5	07mlv5 vibrio vuln	372	76.5	6.4	538	2	09PIV5	09piv5 campylobact
300	77.5	6.5	1476	2	08ST66	08st66 dictyostel	373	76.5	6.4	555	2	08NBG4	08nbg4 homo sapien
301	77.5	6.5	1784	2	025377	025377 loligo opal	374	76.5	6.4	570	2	07Z6C6	07z6c6 homo sapien
302	77.5	6.5	2141	2	0869H2	0869h2 lymnaea sta	375	76.5	6.4	589	2	09ZLNL1	09zlnl1 helicobacte
303	77	6.4	170	2	072UC4	072uc4 leptospira	376	76.5	6.4	614	2	08FWB2	08fw2 bruceila su
304	77	6.4	255	2	08FOO4	08foo4 leptospira	377	76.5	6.4	649	2	06KZL4	06kzl4 picrophilus
305	77	6.4	255	2	098VNS	098vns equine arte	378	76.5	6.4	687	2	074520	074520 echizosacch
306	77	6.4	286	2	061082	061082 bacillus an	379	76.5	6.4	743	2	08XN80	08xn80 clostridium
307	77	6.4	286	2	073A28	073a28 bacillus ce	380	76.5	6.4	839	2	0918C9	0918c9 gallus gall
308	77	6.4	333	1	09XTH3	09xth3 caenorhabdi	381	76.5	6.4	909	2	08T9W6	08t9w6 dictyostella
309	77	6.4	353	2	MLIA_MOUSE	061184 mus musculu	382	76.5	6.4	1485	2	08EU2A	08eu2a mycoplasma
310	77	6.4	379	2	08WER6	08wer6 thomomys ta	383	76.5	6.4	1641	2	06BS27	06bs27 debaryomyce
311	77	6.4	383	2	08TZC2	08tzc2 methanopyru	384	76.5	6.4	156	2	081504	081504 hepatitis c
312	77	6.4	386	2	07MXO0	07mxo0 porphyromon	385	76.5	6.4	201	2	06MT09	06mt09 mycoplasma
313	77	6.4	419	2	P94949	P94949 methanopyru	386	76.5	6.4	210	2	06PX10	06px10 methanosarc
314	77	6.4	423	2	071X58	071x58 listeria mo	387	76.5	6.4	255	2	06V715	06v715 equine arte
315	77	6.4	430	2	08U1Z6	08u1z6 treponema d	388	76.5	6.4	272	2	08R7J2	08r7j2 thermoaer
316	77	6.4	435	2	073RD9	073rd9 treponema d	389	76.5	6.4	292	2	08ELU4	08elu4 oceanobacil
317	77	6.4	444	2	08NYSX	08nysx staphylococ	390	76.5	6.4	325	2	09Z2H9	09z2h9 mesocricetu
318	77	6.4	444	2	06CD70	06cd70 staphylococ	391	76.5	6.4	342	1	NUSM_LOCM1	09z426 locusta mig
319	77	6.4	490	2	014670	014670 homo sapien	392	76.5	6.4	402	2	021933	021933 caenorhabdi
320	77	6.4	491	2	09T251	09t251 phytophthor	393	76.5	6.4	425	2	09HRS7	09hrs7 actinobacil
321	77	6.4	519	2	09ASQ7	09asq7 arabadopsis	394	76.5	6.4	438	2	08BHG2	08bh2 pseudomonas
322	77	6.4	559	2	09AAX4	09aax4 caulobacter	395	76.5	6.4	461	2	085002	085002 streptococ
323	77	6.4	590	1	NUSM_TRYBB	P04540 trypanosoma	396	76.5	6.4	474	2	07ZSX4	07zsx4 leptospira

397	76	6.4	474	2	Q8F2K0	Q8F2K0 leptoplia	470	75	6.3	132	2	Q6N505	Q6N505 rhodopseudo
398	76	6.4	519	2	Q852P3	Q852P3 perilla fru	471	75	6.3	156	2	Q81498	Q81498 hepatitis c
399	76	6.4	567	2	Q6NXT6	Q6NXT6 homo sapien	472	75	6.3	156	2	Q81507	Q81507 hepatitis c
400	76	6.4	616	2	Q7QWH6	Q7QWH6 giardia lam	473	75	6.3	156	2	Q81531	Q81531 hepatitis c
401	76	6.4	669	2	Q9LZ27	Q9LZ27 arabidopsis	474	75	6.3	215	2	Q34238	Q34238 capricornis
402	76	6.4	699	2	Q6LVM6	Q6LVM6 uncultured	475	75	6.3	218	2	Q6SKR1	Q6SKR1 arthobacte
403	76	6.4	851	2	Q6CK04	Q6CK04 kluyveromyc	476	75	6.3	225	2	Q6VMD0	Q6VMD0 avian infec
404	76	6.4	931	2	Q7NBN0	Q7NBN0 mycoplasma	477	75	6.3	227	2	Q9GAT3	Q9GAT3 ochotona hy
405	76	6.4	1252	1	Q7PVU9	Q7PVU9 anopheles g	478	75	6.3	249	1	YD68 METJA	YD68 METJA methanococ
406	76	6.4	1301	1	Q8X9 CAEBL	Q8X9 CAEBL caenorhabdi	479	75	6.3	256	2	Q631U3	Q631U3 bacillus ce
407	76	6.4	1450	1	QCTR_RABIT	Q00554 oryctolagus	480	75	6.3	274	2	Q9KND0	Q9KND0 vibrio chol
408	76	6.4	1481	2	Q9TX9	Q9TX9 oryctolagus	481	75	6.3	277	2	Q6MNA3	Q6MNA3 bdellovibri
409	76	6.4	1551	2	Q96WNA4	Q96WNA4 venturia in	482	75	6.3	294	2	Q8RST4	Q8RST4 fusobacteri
410	76	6.4	1783	2	Q18698	Q18698 caenorhabdi	483	75	6.3	302	2	Q6CWK2	Q6CWK2 kluyveromyc
411	76	6.4	1877	2	Q8MOA1	Q8MOA1 caenorhabdi	484	75	6.3	330	2	Q58239	Q58239 pyrococcus
412	76	6.4	2009	2	Q7RBP2	Q7RBP2 plasmodium	485	75	6.3	371	2	Q8BW45	Q8BW45 mus musculu
413	76	6.4	3010	2	Q90191	Q90191 hepatitis c	486	75	6.3	373	1	PE23 PTG	PE23 PTG scrofa
414	76	6.4	3010	2	Q90193	Q90193 hepatitis c	487	75	6.3	380	1	CYB_RANRU	CYB_RANRU rana rugosa
415	76	6.4	3010	2	Q90194	Q90194 hepatitis c	488	75	6.3	380	2	Q6G6U2	Q6G6U2 nandus nebu
416	75.5	6.3	156	1	ML1A RAT	P49218 rattus norv	489	75	6.3	387	2	Q46657	Q46657 sus scrofa
417	75.5	6.3	162	2	Q66PG7	Q66PG7 rattus norv	490	75	6.3	407	2	Q7NRF5	Q7NRF5 chromobacte
418	75.5	6.3	220	2	Q633A3	Q633A3 bacillus th	491	75	6.3	418	2	Q6ORF8	Q6ORF8 legionella
419	75.5	6.3	228	2	Q9VUN8	Q9VUN8 drosophila	492	75	6.3	418	2	Q6A8T1	Q6A8T1 propionibac
420	75.5	6.3	231	2	Q6MD11	Q6MD11 paracitlamyd	493	75	6.3	460	2	Q62CR6	Q62CR6 burkholderi
421	75.5	6.3	244	2	Q6B927	Q6B927 graciilaria	494	75	6.3	460	2	Q63QA3	Q63QA3 burkholderi
422	75.5	6.3	247	2	Q7TP13	Q7TP13 rattus norv	495	75	6.3	473	1	GAR1 HUMAN	P24046 homo sapien
423	75.5	6.3	248	2	Q63E29	Q63E29 bacillus ce	496	75	6.3	488	2	Q7RWS8	Q7RWS8 neurospora
424	75.5	6.3	248	2	Q6HMF5	Q6HMF5 bacillus th	497	75	6.3	498	2	Q7SU67	Q7SU67 fugu rubrip
425	75.5	6.3	263	2	Q63GB2	Q63GB2 bacillus ce	498	75	6.3	526	2	Q9SN21	Q9SN21 arabidopsis
426	75.5	6.3	263	2	Q7PDP2	Q7PDP2 streptococc	499	75	6.3	543	2	Q7NS50	Q7NS50 chromobacte
427	75.5	6.3	263	2	Q81YU8	Q81YU8 bacillus an	500	75	6.3	619	2	Q34952	Q34952 bacillus su
428	75.5	6.3	263	2	Q8CYF4	Q8CYF4 streptococc	501	75	6.3	662	2	Q7VED4	Q7VED4 prochloroco
429	75.5	6.3	263	2	Q6HNS6	Q6HNS6 bacillus th	502	75	6.3	753	2	Q98S90	Q98S90 guillardia
430	75.5	6.3	269	2	Q66PG6	Q66PG6 xenopus lae	503	75	6.3	777	2	Q6BG55	Q6BG55 paramecium
431	75.5	6.3	278	2	Q865K7	Q865K7 macropus eu	504	75	6.3	885	2	Q8PUL6	Q8PUL6 methanobarc
432	75.5	6.3	303	2	Q9KZ08	Q9KZ08 streptomyce	505	75	6.3	937	2	Q82ZR7	Q82ZR7 enterococc
433	75.5	6.3	310	2	Q87OH5	Q87OH5 escherichia	506	75	6.3	1008	2	Q89152	Q89152 hepatitis c
434	75.5	6.3	326	2	Q9ESJ3	Q9ESJ3 rattus norv	507	75	6.3	1008	2	Q89153	Q89153 hepatitis c
435	75.5	6.3	339	2	Q9KSJ3	Q9KSJ3 vibrio chol	508	75	6.3	1082	2	Q89156	Q89156 hepatitis c
436	75.5	6.3	342	2	Q9QEV3	Q9QEV3 human herpe	509	75	6.3	1131	2	Q8NAT5	Q8NAT5 homo sapien
437	75.5	6.3	352	1	RNFD_ECOLI	P58125 escherichia	510	75	6.3	1145	2	Q8GUB7	Q8GUB7 gymdocoea n
438	75.5	6.3	352	1	RNFD_ECOLI	P76182 escherichia	511	75	6.3	1154	2	Q6PRT6	Q6PRT6 escherich
439	75.5	6.3	352	1	RNFD_ECOLI	Q81H94 escherichia	512	75	6.3	1336	2	Q6F1U1	Q6F1U1 mesoplasma
440	75.5	6.3	352	2	Q83KY5	Q83KY5 shigella fl	513	75	6.3	1704	2	Q95206	Q95206 trypanosoma
441	75.5	6.3	379	1	CYB_ZAPTR	Q9XN1 zapus trino	514	75	6.3	2248	1	CYAL DROME	P32870 drosophila
442	75.5	6.3	389	2	Q8AVS5	Q8AVS5 hyala japoni	515	75	6.3	2248	2	Q9VY17	Q9VY17 drosophila
443	75.5	6.3	397	2	Q9NARS	Q9NARS caenorhabdi	516	75	6.3	3010	2	Q68833	Q68833 hepatitis c
444	75.5	6.3	397	2	Q6RXC2	Q6RXC2 human cytom	517	75	6.3	3010	2	Q9J3G2	Q9J3G2 hepatitis c
445	75.5	6.3	410	2	Q7ONM4	Q7ONM4 strongyloid	518	75	6.3	3010	2	Q9J3G5	Q9J3G5 hepatitis c
446	75.5	6.3	415	1	TNAB_ECO57	Q8XB33 escherichia	519	75	6.3	3010	2	Q9Q1Y7	Q9Q1Y7 hepatitis c
447	75.5	6.3	415	1	TNAB_ECOLI	P31173 escherichia	520	75	6.3	3010	2	Q9Q1Y8	Q9Q1Y8 hepatitis c
448	75.5	6.3	415	2	Q8FBV1	Q8FBV1 escherichia	521	74.5	6.2	174	2	P97068	P97068 salmonella
449	75.5	6.3	433	2	Q6FIC9	Q6FIC9 caenorhabdi	522	74.5	6.2	179	2	Q8BPH9	Q8BPH9 oceanobacil
450	75.5	6.3	446	2	Q7S8U0	Q7S8U0 neurospora	523	74.5	6.2	180	2	P71253	P71253 escherichia
451	75.5	6.3	471	1	SH2A_MOUSE	P35363 mus musculu	524	74.5	6.2	227	2	Q9GAT4	Q9GAT4 ochotona cu
452	75.5	6.3	481	2	Q8COK0	Q8COK0 mus musculu	525	74.5	6.2	227	2	Q9GAT5	Q9GAT5 ochotona th
453	75.5	6.3	482	2	Q9P6J0	Q9P6J0 eschizosach	526	74.5	6.2	227	2	Q9GAT6	Q9GAT6 ochotona pr
454	75.5	6.3	491	2	Q6SMJ1	Q6SMJ1 human cytom	527	74.5	6.2	258	2	Q8BWC7	Q8BWC7 lactobacilli
455	75.5	6.3	491	2	Q6SMS4	Q6SMS4 human cytom	528	74.5	6.2	276	2	Q9R905	Q9R905 rhizobium m
456	75.5	6.3	491	2	Q6SMW2	Q6SMW2 human cytom	529	74.5	6.2	280	2	Q6WTF6	Q6WTF6 synchococc
457	75.5	6.3	491	2	Q6SMW1	Q6SMW1 human cytom	530	74.5	6.2	290	2	Q6SEU1	Q6SEU1 uncultured
458	75.5	6.3	491	2	Q6SMW1	Q6SMW1 human cytom	531	74.5	6.2	298	2	Q6BWD3	Q6BWD3 debaryomyce
459	75.5	6.3	508	2	Q47543	Q47543 chlamydomon	532	74.5	6.2	313	2	Q8RTK6	Q8RTK6 thermotoga
460	75.5	6.3	551	2	Q6CHZ5	Q6CHZ5 yarrowia li	533	74.5	6.2	335	2	Q9KX57	Q9KX57 thermotoga
461	75.5	6.3	551	1	PVR2_MOUSE	Q91X65 mus musculu	534	74.5	6.2	355	1	C3X1 HUMAN	P49238 homo sapien
462	75.5	6.3	593	2	Q2S372	Q2S372 helicobacte	535	74.5	6.2	354	2	Q81YV2	Q81YV2 plasmodium
463	75.5	6.3	708	2	Q22806	Q22806 caenorhabdi	536	74.5	6.2	377	2	Q76WV3	Q76WV3 varigula hil
464	75.5	6.3	746	2	Q8PGM4	Q8PGM4 xanthomonas	537	74.5	6.2	378	2	Q6D0V8	Q6D0V8 brassica na
465	75.5	6.3	773	2	Q963K5	Q963K5 arabidopsis	538	74.5	6.2	379	1	CYB_OCHPR	Q963K5 arabidopsis
466	75.5	6.3	1008	2	CLCA_ARATH	P92941 arabidopsis	539	74.5	6.2	379	2	Q8WB05	Q8WB05 apidontia pr
467	75.5	6.3	1142	2	Q89154	Q89154 hepatitis c	540	74.5	6.2	379	2	Q9B9E3	Q9B9E3 chaetodipus
468	75.5	6.3	1583	2	Q9P984	Q9P984 schizosach	541	74.5	6.2	392	2	Q9LNC4	Q9LNC4 micromospis
469	75.5	6.3	3010	2	Q9J3G7	Q9J3G7 hepatitis c	542	74.5	6.2	442	2	Q94AI3	Q94AI3 arabidopsis

543	74.5	6.2	456	2	065MD8	065md8 bacillus li	616	74	6.2	650	2	0956S6	0956s6 lactococcus
544	74.5	6.2	471	1	5H2A_RAT	P14842 rectus norv	617	74	6.2	742	2	06FNW6	06fnw6 candida gla
545	74.5	6.2	473	2	06K5T9	06k5t9 bacillus ha	618	74	6.2	841	2	09AHP1	09ahp1 carsonella
546	74.5	6.2	488	2	06QV71	06qv71 aspergillus	619	74	6.2	846	2	093U47	093u47 carsonella
547	74.5	6.2	500	2	024348	024348 sorghum bic	620	74	6.2	892	2	08TGB2	08tgb2 candida alb
548	74.5	6.2	540	2	066CQ5	066cq5 arabidopsis	621	74	6.2	1133	2	095S39	095s39 arabidopsis
549	74.5	6.2	562	2	08N2S3	08n2s3 homo sapien	622	74	6.2	1123	2	09SPU7	09spu7 arabidopsis
550	74.5	6.2	574	2	022454	022454 triticum ae	623	74	6.2	3010	2	0913V3	0913v3 hepatitis c
551	74.5	6.2	597	2	03VDA0	03vda0 dtiosophila	624	74	6.2	3010	2	09DPE8	09dpe8 hepatitis c
552	74.5	6.2	618	1	YKR4_YEAST	P36029 saccharomyc	625	74	6.2	3010	2	09UJH6	09ujh6 hepatitis c
553	74.5	6.2	848	1	08VVK9	08vvk9 corynebacte	626	74	6.2	3010	2	09Q1Y1	09q1y1 hepatitis c
554	74.5	6.2	990	1	FTSK_VIBVU	06d8m2 vibrio vuln	627	74	6.2	3010	2	09Q1Y2	09q1y2 hepatitis c
555	74.5	6.2	1033	2	07Z2C1	07z2c1 typanosoma	628	74	6.2	120	2	09SKA6	09ska6 arabidopsis
556	74.5	6.2	1034	2	07Z2C0	07z2c0 typanosoma	629	73.5	6.2	153	2	092XD3	092xd3 pyrobaculum
557	74.5	6.2	1183	2	094447	094447 galliphora	630	73.5	6.2	180	2	08ZXS3	08zxs3 pyrobaculum
558	74.5	6.2	1520	2	08T687	08t687 dictyostell	631	73.5	6.2	180	2	P712S1	P712s1 escherichia
559	74.5	6.2	1559	2	07S0S1	07s0s1 neurospora	632	73.5	6.2	180	2	P712S7	P712s7 escherichia
560	74.5	6.2	1808	2	09LYS6	09lys6 arabidopsis	633	73.5	6.2	180	2	P75018	P75018 escherichia
561	74.5	6.2	1837	2	08IKP1	08ikf1 plasmodium	634	73.5	6.2	199	2	08DVR3	08dvr3 streptococc
562	74.5	6.2	3010	2	091AU0	091au0 hepatitis c	635	73.5	6.2	216	1	YK36_AQUAE	067827 aquilex aeo
563	74	6.2	124	2	08KC46	08kc46 chlorobium	636	73.5	6.2	226	2	09J0X1	09j0x1 avian infec
564	74	6.2	156	2	081528	081528 hepatitis c	637	73.5	6.2	270	2	08HBP0	08hbp0 perognathus
565	74	6.2	167	2	08W272	08w272 homo sapien	638	73.5	6.2	270	2	08HIY6	08hiy6 perognathus
566	74	6.2	225	2	091SA2	091sa2 avian infec	639	73.5	6.2	274	2	095L51	095l51 capra hircu
567	74	6.2	230	2	088Y70	088y70 lactobacill	640	73.5	6.2	298	2	06Z2T3	06z2t3 oryza sativ
568	74	6.2	231	1	028852	027961 archaeoglob	641	73.5	6.2	318	2	055895	055895 synechocyst
569	74	6.2	231	2	028852	028892 archaeoglob	642	73.5	6.2	338	1	YYAD_BACSU	037520 bacillus su
570	74	6.2	238	2	06HER1	06het1 bacillus th	643	73.5	6.2	360	2	08UW8	08uw8 bractydantio
571	74	6.2	255	2	066483	066483 equine arte	644	73.5	6.2	367	2	064BD6	064bd6 uncultured
572	74	6.2	278	2	06CUI8	06cul8 kluyveromyc	645	73.5	6.2	379	1	CYB_PHOGR	035457 phoca green
573	74	6.2	286	1	POTB_MYCPN	P75058 mycoplasma	646	73.5	6.2	379	1	CYB_THOTA	048001 thomomys ca
574	74	6.2	291	2	066958	066958 yerania ps	647	73.5	6.2	379	2	09G3M8	09g3m8 ochotona cu
575	74	6.2	294	2	09SM72	09sm72 oryza sativ	648	73.5	6.2	380	1	CYB_STRPU	P15547 strongyloce
576	74	6.2	295	1	CYOE_PSEPU	06wm75 pseudomonas	649	73.5	6.2	384	1	OPGC_SALTY	082719 salmonella
577	74	6.2	295	2	06S4M3	06s4m3 pseudomonas	650	73.5	6.2	385	2	P94442	P94442 bacillus su
578	74	6.2	300	1	NUZM_ASCSU	P48777 ascaria suu	651	73.5	6.2	387	2	09KMU2	09kmw2 sphingomona
579	74	6.2	312	1	PYRB_AERPE	09ch74 aeropyrum p	652	73.5	6.2	387	2	07MVX5	07mvx5 porphyromon
580	74	6.2	312	2	09CH74	09ch74 lactococcus	653	73.5	6.2	389	1	OXNR_MACMU	P64494 macaca mula
581	74	6.2	315	2	0710S2	0710s2 epialax leuc	654	73.5	6.2	391	1	OXNR_BOVIN	P64449 bos taurus
582	74	6.2	321	2	08M6V0	08m6v0 ligilopys j	655	73.5	6.2	397	2	0822F7	0822f7 enterococcu
583	74	6.2	324	2	08DVZ6	08dvz6 streptococc	656	73.5	6.2	409	2	07V1A0	07v1a0 prochloroco
584	74	6.2	349	1	110S_MOUSE	061190 mus musculu	657	73.5	6.2	413	2	09Z8T3	09z8t3 listeria in
585	74	6.2	350	1	MLIA_HUMAN	P48039 homo sapien	658	73.5	6.2	421	2	08PK37	08pk37 xenomomas
586	74	6.2	351	2	09VM77	09vm77 mus musculu	659	73.5	6.2	425	2	06DEK1	06dek1 ertwinia car
587	74	6.2	354	2	06SUT4	06sut4 manheimia	660	73.5	6.2	442	2	08GZJ4	08gzj4 arabidopsis
588	74	6.2	361	2	064AL9	06e4l9 uncultured	661	73.5	6.2	442	2	09X1Q7	09x1q7 arabidopsis
589	74	6.2	379	1	CYB_THOMO	06wek2 thomomys mo	662	73.5	6.2	491	1	VIE1_HCMVA	P13202 human cytom
590	74	6.2	379	2	047980	047980 thomomys bo	663	73.5	6.2	491	2	06SNZ8	06snz8 human cytom
591	74	6.2	379	2	048002	048002 thomomys mo	664	73.5	6.2	491	2	07M6S4	07m6s4 human cytom
592	74	6.2	379	2	048003	048003 thomomys mo	665	73.5	6.2	491	2	07M6S4	07m6s4 human cytom
593	74	6.2	379	2	08WEK5	08wek5 thomomys ca	666	73.5	6.2	518	2	07RT44	07rt44 plasmodium
594	74	6.2	380	2	08HHU7	08hhj7 thomomys bo	667	73.5	6.2	523	2	064WY6	064wy6 bacteroides
595	74	6.2	380	2	074KX0	074kx0 lactobacill	668	73.5	6.2	557	2	08VZ62	08vz62 arabidopsis
596	74	6.2	381	1	CYB_PSENI	035553 pseudantech	669	73.5	6.2	574	2	093990	093990 candida alb
597	74	6.2	396	2	08NKC4	08nkc4 strephyloloc	670	73.5	6.2	607	2	06DFU5	06dfu5 xenopus lae
598	74	6.2	396	2	093V76	093v76 strephyloloc	671	73.5	6.2	634	1	KUP_XYLPA	09pc78 xyella fas
599	74	6.2	396	2	07A6D3	07a6d3 strephyloloc	672	73.5	6.2	637	1	MUTL_BACHD	09kact bacillus ha
600	74	6.2	396	2	06GARI	06gari strephyloloc	673	73.5	6.2	640	1	APRN_ENTHI	P20301 entamoeba h
601	74	6.2	396	2	06G168	06g168 strephyloloc	674	73.5	6.2	653	2	08TTH1	08tth1 methanosarc
602	74	6.2	418	2	06QF89	06qf89 legionella	675	73.5	6.2	668	2	068468	068468 corynebacte
603	74	6.2	418	2	06QFCS	06qfcs legionella	676	73.5	6.2	731	2	016531	016531 caenorhabdi
604	74	6.2	418	2	06QF07	06qf07 legionella	677	73.5	6.2	846	2	093U53	093u53 carsonella
605	74	6.2	442	2	09CEB6	09ceb6 lactococcus	678	73.5	6.2	1049	2	06FMY2	06fmy2 candida gla
606	74	6.2	457	2	08RBZ7	08rbz7 thermoaer	679	73.5	6.2	1095	2	09CTH5	09cth5 arabidopsis
607	74	6.2	475	2	09X2G7	09x2g7 streptomyc	680	73.5	6.2	1174	2	07M006	07m006 murine hepa
608	74	6.2	485	2	09XVK0	09xvk0 caenorhabdi	681	73.5	6.2	1277	2	076G00	07yus9 drosophila
609	74	6.2	487	2	023384	023384 arabidopsis	682	73.5	6.2	1287	2	09UW51	09uw51 drosophila
610	74	6.2	493	2	09EVJ7	09evj7 flavobacter	683	73.5	6.2	1287	2	09V124	09v124 drosophila
611	74	6.2	503	2	06M052	06m052 methanococc	684	73.5	6.2	1287	2	09V124	09v124 drosophila
612	74	6.2	528	2	06CKX2	06ckx2 kluyveromyc	685	73.5	6.2	1292	2	09A1H0	09a1h0 carsonella
613	74	6.2	528	2	07O1Q9	07o1q9 kluyveromyc	686	73.5	6.2	1476	2	0965D3	0965d3 dictyostell
614	74	6.2	540	2	06LFP3	06lfp3 plasmodium	687	73.5	6.2	1545	2	08GU65	08gu65 oryza sativ
615	74	6.2	581	2	06FIT6	06fit6 candida gla	688	73.5	6.2	2666	2	06FW99	06fw99 candida gla

589	73.5	6.2	3010	2	Q9DTE6	Q9dte6 hepatitis c	762	73	6.1	668	2	Q9ALX8	Q9alx8 burkholderi
590	73.5	6.2	3381	2	Q8IDK4	Q8idk4 plasmodium	763	73	6.1	668	2	Q63JL61	Q63jl61 burkholderi
591	73.5	6.2	4470	2	Q66WN5	Q66wn5 murine hepa	764	73	6.1	676	2	Q9VF31	Q9v31 drosophila
592	73.5	6.2	7176	1	R1AB_CWMA5	R16342 m replicase	765	73	6.1	788	1	FTSK_STAM	P64164 staphylococ
593	73.5	6.2	7178	2	Q66WN6	Q66wn6 murine hepa	766	73	6.1	788	1	FTSK_STAM	P64165 staphylococ
594	73	6.1	114	2	Q75XA7	Q75xa7 helicobacte	767	73	6.1	789	2	Q6GHF9	Q6ghf9 staphylococ
595	73	6.1	114	2	Q92LU2	Q92lu2 helicobacte	768	73	6.1	832	2	Q7UQP9	Q7uq9 rhodospirill
596	73	6.1	138	2	Q97777	Q97777 elephas max	769	73	6.1	844	2	Q6KYT8	Q6kyt8 picophilus
597	73	6.1	140	2	Q64145	Q64145 rattus sp.	770	73	6.1	861	2	Q9AVX8	Q9avx8 guilliaridia
598	73	6.1	145	2	Q9UX80	Q9ux80 bulfolobus	771	73	6.1	966	1	PKD2_MOUSE	Q35245 mus musculu
599	73	6.1	155	2	Q7VJPI	Q7vjpi helicobacte	772	73	6.1	966	2	Q7TSI7	Q7tsi7 mus musculu
700	73	6.1	156	2	Q81510	Q81510 hepatitis c	773	73	6.1	966	2	Q8BPR6	Q8bpr6 mus musculu
701	73	6.1	156	2	Q81522	Q81522 hepatitis c	774	73	6.1	971	2	Q60337	Q60337 homo sapien
702	73	6.1	156	2	Q81537	Q81537 hepatitis c	775	73	6.1	1035	2	Q967W1	Q967w1 archistoboma
703	73	6.1	163	2	Q80RY8	Q80ry8 avian infec	776	73	6.1	1075	2	Q9LPE2	Q9lpe2 arabidopsis
704	73	6.1	220	2	Q72Z40	Q72z40 bacillus ce	777	73	6.1	1111	2	Q86FP2	Q86fp2 caenorhabdi
705	73	6.1	223	1	VME1_IBVG	Q910e2 avian infec	778	73	6.1	1137	2	Q9N323	Q9n323 caenorhabdi
706	73	6.1	223	2	Q91S57	Q91s57 avian infec	779	73	6.1	1931	2	Q8RJT3	Q8rjt3 stigmatella
707	73	6.1	226	2	Q7TPP6	Q7tp6 avian infec	780	73	6.1	2010	2	Q7PEZ7	Q7pe7 anopheles g
708	73	6.1	238	1	PYRF_BACCR	Q819e6 bacillus ce	781	73	6.1	3010	2	P88803	P88803 hepatitis c
709	73	6.1	238	2	Q636E3	Q636e3 bacillus ce	782	73	6.1	3010	2	Q9J3G1	Q9j3g1 hepatitis c
710	73	6.1	238	2	Q73216	Q73216 bacillus ce	783	73	6.1	3010	2	Q9J3I0	Q9j3i0 hepatitis c
711	73	6.1	249	2	Q9PDU6	Q9pdu6 streptococc	784	73	6.1	3013	2	Q9QIX9	Q9qix9 hepatitis c
712	73	6.1	255	2	P87639	P87639 equine arte	785	73	6.1	3013	2	Q9QIX9	Q9qix9 hepatitis c
713	73	6.1	255	2	Q9YNU0	Q9ynu0 equine arte	786	73	6.1	6875	2	Q28733	Q28733 oryctolagus
714	73	6.1	261	2	Q7QN39	Q7qn39 anopheles g	787	73	6.1	156	2	Q81516	Q81516 hepatitis c
715	73	6.1	264	2	Q7M552	Q7m552 vibrio vuln	788	72.5	6.1	156	2	Q81519	Q81519 hepatitis c
716	73	6.1	264	2	Q8DAQ9	Q8daq9 vibrio vuln	789	72.5	6.1	173	2	Q9MD17	Q9md17 equine arte
717	73	6.1	279	2	Q6TY95	Q6ty95 xiphinema a	790	72.5	6.1	174	2	P97065	P97065 salmonella
718	73	6.1	282	1	NU2M_CAEEL	P24889 caenorhabdi	791	72.5	6.1	180	2	P71252	P71252 escherichia
719	73	6.1	290	2	Q8NX00	Q8nx00 staphylococ	792	72.5	6.1	180	2	P71252	P71252 escherichia
720	73	6.1	290	2	Q6G9W4	Q6g9w4 staphylococ	793	72.5	6.1	180	2	P71255	P71255 escherichia
721	73	6.1	295	2	Q8VU02	Q8vu02 pseudomonas	794	72.5	6.1	180	2	P71256	P71256 escherichia
722	73	6.1	295	2	Q88PN3	Q88pn3 pseudomonas	795	72.5	6.1	180	2	P71258	P71258 escherichia
723	73	6.1	303	2	Q94EJ0	Q94ej0 arabidopsis	796	72.5	6.1	180	2	P71259	P71259 escherichia
724	73	6.1	314	2	Q8ESH3	Q8esh3 oceanobacil	797	72.5	6.1	180	2	P71260	P71260 escherichia
725	73	6.1	322	2	Q9H6T9	Q9het9 homo sapien	798	72.5	6.1	180	2	P71261	P71261 escherichia
726	73	6.1	326	2	Q99NR7	Q99nr7 muscardinus	799	72.5	6.1	191	2	Q8U4P0	Q8u4p0 pyrococcus
727	73	6.1	335	2	Q8SML8	Q8sml8 escherichia	800	72.5	6.1	208	2	Q63447	Q63447 echinotrix
728	73	6.1	339	1	SRG7_CAEEL	P54129 caenorhabdi	801	72.5	6.1	208	2	Q7J7L2	Q7j7l2 echinotrix
729	73	6.1	340	2	Q9N2T2	Q9n2c2 caenorhabdi	802	72.5	6.1	209	2	Q7J7L0	Q7j7l0 echinotrix
730	73	6.1	343	2	Q7YFU0	Q7yfu0 myrmica bul	803	72.5	6.1	209	2	Q8GZ10	Q8gz10 arabidopsis
731	73	6.1	343	2	Q8SAS7	Q8saa7 una scopari	804	72.5	6.1	209	2	Q49634	Q49634 mycobacteri
732	73	6.1	348	2	Q9TD49	Q9td49 cyrtolobias	805	72.5	6.1	210	2	Q7J7J9	Q7j7j9 echinotrix
733	73	6.1	364	1	GHSR_MOUSE	Q99p50 mus musculu	806	72.5	6.1	211	2	Q7J7L3	Q7j7l3 echinotrix
734	73	6.1	364	1	GHSR_RAT	Q08725 rattus norv	807	72.5	6.1	214	2	Q63950	Q63950 echinotrix
735	73	6.1	375	2	Q86NC0	Q86nc0 caenorhabdi	808	72.5	6.1	217	2	Q9XMK7	Q9xmk7 ochotona pr
736	73	6.1	378	2	Q70BC4	Q70eg5 saccosctomus	809	72.5	6.1	224	2	Q8RGE6	Q8rge6 fusobacteri
737	73	6.1	378	2	Q70EG5	Q70eg5 saccosctomus	810	72.5	6.1	225	2	Q7M2C0	Q7m2c0 leishmania
738	73	6.1	379	1	CYB_CRATU	Q8wdv6 cratogeomys	811	72.5	6.1	259	2	Q8RES9	Q8res9 fusobacteri
739	73	6.1	379	2	Q8MDV7	Q8mdv7 cratogeomys	812	72.5	6.1	285	2	Q86DD6	Q86dd6 caenorhabdi
740	73	6.1	379	2	Q34039	Q34039 cratogeomys	813	72.5	6.1	291	2	Q24561	Q24561 zea mays (m
741	73	6.1	379	2	Q69802	Q69802 cratogeomys	814	72.5	6.1	298	2	Q8R2A8	Q8r2a8 mus musculu
742	73	6.1	383	2	Q9GL20	Q9gl20 cyrtolobias	815	72.5	6.1	308	2	Q6M472	Q6m472 rhodopsendo
743	73	6.1	391	1	Y450_BUCAP	Q8K999 buchneria ap	816	72.5	6.1	309	2	Q7I0E1	Q7iue1 bos taurus
744	73	6.1	394	2	Q6EEB9	Q6ee99 latimeria c	817	72.5	6.1	315	2	Q91G02	Q91g02 arabidopsis
745	73	6.1	399	2	Q6LOJ3	Q6l0j3 picophilus	818	72.5	6.1	320	1	QXAZ_LACIA	Q9ch39 lactococcus
746	73	6.1	401	2	Q6KZX3	Q6kzx3 picophilus	819	72.5	6.1	325	2	Q9CIT9	Q9c39 lactococcus
747	73	6.1	446	2	Q8H9B3	Q8h9b3 brassica ca	820	72.5	6.1	336	2	Q17077	Q17077 caenorhabdi
748	73	6.1	450	1	VELM_EHY1B	P28948 equine hezp	821	72.5	6.1	348	2	Q99924	Q99924 enterococu
749	73	6.1	450	2	Q6DLF9	Q6dlf9 equid hezpe	822	72.5	6.1	348	2	Q833B9	Q833b9 enterococu
750	73	6.1	453	2	Q6S6V2	Q6s6v2 equid hezpe	823	72.5	6.1	350	2	Q835L2	Q835l2 enterococu
751	73	6.1	453	2	Q94307	Q94307 caenorhabdi	824	72.5	6.1	356	2	Q8FYM4	Q8fym4 bruceella su
752	73	6.1	461	2	Q9R923	Q9r923 streptococc	825	72.5	6.1	363	2	Q70US3	Q70us3 dirofilaria
753	73	6.1	474	2	Q94C17	Q94c17 arabidopsis	826	72.5	6.1	363	2	Q6HGU9	Q6hgu9 bacillus th
754	73	6.1	487	2	Q7MBA5	Q7mba5 photorhabdu	827	72.5	6.1	374	2	Q8MKR0	Q8mkr0 ovis aries
755	73	6.1	494	1	KCF1_HUMAN	Q9h3mo homo sapien	828	72.5	6.1	379	1	CYB_OCHAL	Q9gby1 ochotona cu
756	73	6.1	510	2	Q27072	Q27072 taenia soli	829	72.5	6.1	379	1	CYB_OCHCU	Q9g1b9 ochotona cu
757	73	6.1	553	2	Q9ZJY5	Q9zjy5 helicobacte	830	72.5	6.1	379	1	CYB_OCHHI	Q9gby6 ochotona hi
758	73	6.1	556	2	Q7QZJ9	Q7qzj9 gardia lam	831	72.5	6.1	379	1	CYB_OCHHY	Q9g662 ochotona hy
759	73	6.1	615	2	Q6BIO1	Q6bi01 debaryomyce	832	72.5	6.1	379	1	CYB_OCHKO	Q9gpb0 ochotona ko
760	73	6.1	635	2	Q86X77	Q86x77 homo sapien	833	72.5	6.1	379	1	CYB_OCHNB	Q9gpb2 ochotona nu
761	73	6.1	643	2	Q7NBK6	Q7nbk6 mycoplasma	834	72.5	6.1	379	1	CYB_OCHRO	Q9gpb5 ochotona ro

835	72.5	6.1	379	1	CYB_OCHRU	093uz1 ochotona ru	908	72	6.0	226	2	07TEH2	07teh2 avian infec
836	72.5	6.1	379	1	CYB_OCHTH	093ub6 ochotona th	909	72	6.0	227	2	07Y6X7	07y6x7 tigrisopus c
837	72.5	6.1	379	1	CYB_OCHTH	093ub7 ochotona th	910	72	6.0	227	2	020551	020551 ursus amerl
838	72.5	6.1	379	1	070UT5	070ut5 ochotona pr	911	72	6.0	229	2	08E9R2	08e9r2 shewanella
839	72.5	6.1	379	2	071IX8	071ix8 ochotona ca	912	72	6.0	249	2	0812U8	0812u8 bacillus ce
840	72.5	6.1	379	2	085AV3	085av3 chlamyrogal	913	72	6.0	254	2	081MK0	081mk0 bacillus an
841	72.5	6.1	379	2	09G1C3	09g1c3 ochotona ca	914	72	6.0	276	2	09HJV7	09hvj7 thermoplas
842	72.5	6.1	379	2	09G1C4	09g1c4 ochotona an	915	72	6.0	279	2	09XXT1	09xxc1 caenorhabd
843	72.5	6.1	379	2	09GAM7	09gam7 chaetodipus	916	72	6.0	286	2	06HKV7	06hk77 bacillus th
844	72.5	6.1	379	2	09GBY2	09gbv2 ochotona ca	917	72	6.0	280	2	06SHA6	06sha6 uncultured
845	72.5	6.1	379	2	09GBY8	09gbv8 ochotona hu	918	72	6.0	303	2	064RZ2	064rz2 bacteroides
846	72.5	6.1	379	2	09GBY9	09gbv9 ochotona hy	919	72	6.0	306	2	06HWV3	06hwv3 bacillus an
847	72.5	6.1	379	2	09GBZ1	09gbz1 ochotona la	920	72	6.0	306	2	08Y980	08y980 listeria mo
848	72.5	6.1	379	2	09GBZ3	09gbz3 ochotona pa	921	72	6.0	306	2	06ODA2	06dda2 lepisosteus
849	72.5	6.1	379	2	08EWI6	08ewi6 mycoplasma	922	72	6.0	311	2	08VRF2	08vrf2 mus musculu
850	72.5	6.1	387	2	06RKP6	06rkp6 human harpe	923	72	6.0	317	2	09CKI6	09cki6 pasteurella
851	72.5	6.1	389	1	0XYR_HUMAN	P30559 homo sapien	924	72	6.0	330	2	07ZUC3	07zuc3 brachydanio
852	72.5	6.1	402	2	08WMQ9	08wmq9 ovis aries	925	72	6.0	333	2	08HTJ9	08htj9 lactobacill
853	72.5	6.1	428	2	066CP9	066cf9 yersteinia ps	926	72	6.0	334	2	088XJ9	088xj9 lactobacill
854	72.5	6.1	428	2	08ZG86	08zgb8 yersteinia pe	927	72	6.0	335	2	09ZYJ2	09zyj2 oryctero
855	72.5	6.1	442	2	06LOY3	06loy3 picrophilus	928	72	6.0	338	2	09XTR2	09xtr2 caenorhabd
856	72.5	6.1	442	2	06PHK5	06phk5 brachydanio	929	72	6.0	339	2	097GD6	097gd6 clostridium
857	72.5	6.1	445	2	06NYH8	06nyh8 brachydanio	930	72	6.0	343	2	085AT6	085at6 uma scopari
858	72.5	6.1	452	2	09T9N6	09t9n6 terebratul	931	72	6.0	343	2	09BAH5	09bah5 uma scopari
859	72.5	6.1	452	2	06P822	06p822 xenopus tro	932	72	6.0	343	2	09TD07	09td07 rachovia ma
860	72.5	6.1	478	2	097OD2	097od2 sulfolobus	933	72	6.0	379	1	CYB_GEOPI	09tex5 geomyx pine
861	72.5	6.1	491	2	06SWI8	06swi8 human cytom	934	72	6.0	379	1	CYB_THOMA	08wek7 thomomyx ma
862	72.5	6.1	499	1	0VIN_AQUAE	067658 aquilex aeo	935	72	6.0	379	2	08R6K4	08r6k4 cratogeomys
863	72.5	6.1	505	2	08ORY6	08ory6 pongine her	936	72	6.0	379	2	08WDV3	08wdv3 cratogeomys
864	72.5	6.1	513	1	PACR_BOVIN	029627 bos taurus	937	72	6.0	379	2	0698Q3	0698q3 cratogeomys
865	72.5	6.1	522	2	023444	023444 caenorhabd	938	72	6.0	379	2	07II09	07iio9 cratogeomys
866	72.5	6.1	526	2	06FDF6	06fdf6 acinetobact	939	72	6.0	379	2	09THD6	09thd6 oryctero
867	72.5	6.1	539	2	07VSI1	07vsi1 bordetella	940	72	6.0	386	1	CYB_SARGL	063848 sarcophyton
868	72.5	6.1	539	2	07W4J6	07w4j6 bordetella	941	72	6.0	391	2	08RLY7	08rly7 salmonella
869	72.5	6.1	539	2	07WFK3	07wfk3 bordetella	942	72	6.0	391	2	08RLY9	08rly9 salmonella
870	72.5	6.1	574	2	06LH28	06lh28 photobacter	943	72	6.0	332	2	09LCN9	09lcn9 micromonosp
871	72.5	6.1	614	2	07U5J3	07u5j3 synechococc	944	72	6.0	336	1	CYB_LAMFL	09cta0 lampetra fl
872	72.5	6.1	635	2	021335	021335 caenorhabd	945	72	6.0	415	1	L52_ADBO5	P03262 human adeno
873	72.5	6.1	660	2	08AW53	08aws3 brachydanio	946	72	6.0	415	1	L52_ADBO5	P04466 human adeno
874	72.5	6.1	661	2	06G4J3	06g4j3 bartonella	947	72	6.0	415	2	06VGJ2	06vgj2 human adeno
875	72.5	6.1	662	2	06G146	06g146 bartonella	948	72	6.0	415	2	071BX5	071bx5 human adeno
876	72.5	6.1	666	1	KUP_STRA3	08e575 streptococc	949	72	6.0	415	2	07M5Z2	07m5z2 human adeno
877	72.5	6.1	671	2	06MCR0	06mcro parachlamyd	950	72	6.0	415	2	07M6J3	07m6j3 human adeno
878	72.5	6.1	688	2	08EKS6	08ek6 shewanella	951	72	6.0	417	2	09NTJ9	09ntj9 homo sapien
879	72.5	6.1	686	2	09TUT2	09tut2 mustela vis	952	72	6.0	418	2	06QRB5	06qrb5 legionella
880	72.5	6.1	717	2	07RICO	07ric0 plasmodium	953	72	6.0	418	2	06QFC3	06qfc3 legionella
881	72.5	6.1	718	2	048872	048872 lactobacill	954	72	6.0	419	2	06GIU4	06giu4 xenopus tro
882	72.5	6.1	734	2	06ZPP2	06zpz2 mus musculu	955	72	6.0	444	1	06GRK5	06grk5 staphylococ
883	72.5	6.1	756	2	08C9E3	08c9e3 mus musculu	956	72	6.0	448	1	INVX_SCHPO	042878 schizosacch
884	72.5	6.1	769	2	09N3Y9	09n3y9 caenorhabd	957	72	6.0	448	2	0460J4	0460j4 drosophila
885	72.5	6.1	832	2	064MT1	064mt1 bacteroides	958	72	6.0	453	2	099XJ2	099xj2 staphylococ
886	72.5	6.1	848	2	08VZH3	08vzh3 arabidopsis	959	72	6.0	453	2	07A8D9	07a8d9 staphylococ
887	72.5	6.1	848	2	09S1U2	09s1u2 arabidopsis	960	72	6.0	453	2	07NWT7	07nwt7 chromobacte
888	72.5	6.1	858	2	0741E5	0741e5 lactobacill	961	72	6.0	465	2	09RDT2	09rdt2 staphylococ
889	72.5	6.1	1103	2	0753W8	0753w8 aabhyra goss	962	72	6.0	468	2	094K50	094k50 arabidopsis
890	72.5	6.1	1304	2	08MNJ0	08mnj0 dictyosteli	963	72	6.0	479	1	COO6_YEAST	P53318 saccharomyc
891	72.5	6.1	1357	2	0817K7	0817k7 caenorhabd	964	72	6.0	497	2	09FV99	09fv99 arabidopsis
892	72.5	6.1	1526	2	019611	019611 caenorhabd	965	72	6.0	518	2	07V0X6	07v0x6 candidatus
893	72.5	6.1	1548	2	070409	07q409 anopheles g	966	72	6.0	523	2	086YB4	086yb4 homo sapien
894	72.5	6.1	1689	2	08QZP4	08qzpf crimean-con	967	72	6.0	530	2	065124	065124 african bwi
895	72.5	6.1	1689	2	09J1H9	09j1h9 crimean-con	968	72	6.0	552	2	06NHU7	06nhu7 corynebacte
896	72.5	6.1	1702	2	095OK2	095qk2 caenorhabd	969	72	6.0	553	2	0975L9	0975l9 lactobolus
897	72.5	6.1	4097	2	07RG07	07rg07 plasmodium	970	72	6.0	556	2	093YH6	093yh6 arabidopsis
898	72.5	6.0	114	2	06VRK9	06vrk9 helicobacte	971	72	6.0	562	2	06CF79	06cf79 yarrowia li
899	72.5	6.0	156	2	081540	081540 hepatis c	972	72	6.0	594	2	07L8K9	07l8k9 homo sapien
900	72.5	6.0	173	2	09WD22	09wd22 equine arte	973	72	6.0	596	2	08R7C9	08r7c9 thermoaer
901	72.5	6.0	173	2	09WD25	09wd25 equine arte	974	72	6.0	600	2	0429J2	0429j2 schizosacch
902	72.5	6.0	182	2	0988T5	0988t5 rhizobium 1	975	72	6.0	610	2	084XZ2	084xz2 tetraselmis
903	72.5	6.0	200	2	041199	041199 porcine rep	976	72	6.0	630	2	024608	024608 dianthus ca
904	72.5	6.0	200	2	09J7J6	09j7j6 porcine rep	977	72	6.0	632	2	06DDJ4	06ddj4 xenopus lae
905	72.5	6.0	209	2	085UJ0	085uj0 ciona savig	978	72	6.0	636	2	0957I9	0957i9 homo sapien
906	72.5	6.0	225	2	06DTU8	06dtu8 avian infec	979	72	6.0	696	2	09UBH6	09ubh6 homo sapien
907	72.5	6.0	225	2	064PZ0	064pfz0 avian infec	980	72	6.0	712	2	094EB6	094ek6 plium baltiv

981	72	6.0	716	2	Q7N732	Q7N732	photorhabdu	1054	71.5	6.0	379	2	Q698Q0	Q698Q0	cratogeomys
982	72	6.0	721	2	Q671A6	Q671A6	symbiobacte	1055	71.5	6.0	379	2	Q71BM1	Q71BM1	glaucomys s
983	72	6.0	736	2	Q7YU76	Q7YU76	dirosophila	1056	71.5	6.0	379	2	Q9TF66	Q9TF66	spermophilu
984	72	6.0	772	2	Q75JF4	Q75JF4	dictyosteli	1057	71.5	6.0	381	2	Q8ZXP7	Q8ZXP7	pyrobaculum
985	72	6.0	788	2	Q8TDO5	Q8TDO5	homo sapien	1058	71.5	6.0	381	2	Q79571	Q79571	musculus ma
986	72	6.0	796	2	Q75D67	Q75D67	ababya goss	1059	71.5	6.0	381	2	Q6RKP4	Q6RKP4	human herpe
987	72	6.0	844	2	Q750H3	Q750H3	ababya goss	1060	71.5	6.0	382	2	Q9N7N8	Q9N7N8	human herpe
988	72	6.0	878	2	Q9VSK2	Q9VSK2	dirosophila	1061	71.5	6.0	383	1	Y1V4_SCHPO	Y1V4_SCHPO	schistosach
989	72	6.0	928	2	Q660E1	Q660E1	borrelia ga	1062	71.5	6.0	386	1	QXYR_PIG	QXYR_PIG	sus scrofa
990	72	6.0	1035	2	Q875W8	Q875W8	saccharomyc	1063	71.5	6.0	386	2	Q8RB76	Q8RB76	thermoanaer
991	72	6.0	1038	1	YKD3_YEAST	P36097	saccharomyc	1064	71.5	6.0	388	2	Q8SQ91	Q8SQ91	myceris th
992	72	6.0	1094	1	PDOD_PLAFK	P30315	plasmodium	1065	71.5	6.0	388	2	Q8SQ93	Q8SQ93	nycteris gr
993	72	6.0	1094	1	Q7KOL4	Q7KOL4	plasmodium	1066	71.5	6.0	390	1	ITR_CARCO	ITR_CARCO	caecomus
994	72	6.0	1113	2	Q9XKX4	Q9XKX4	caenorhabdi	1067	71.5	6.0	392	2	Q9AH88	Q9AH88	streptococc
995	72	6.0	1220	1	PTCI_BRARE	Q98864	brachydanio	1068	71.5	6.0	407	2	Q6DG01	Q6DG01	brachydanio
996	72	6.0	1267	2	Q9U0U5	Q9U0U5	leishmania	1069	71.5	6.0	410	2	Q82AH6	Q82AH6	streptomyce
997	72	6.0	1275	1	TRP_DROME	P19334	dirosophila	1070	71.5	6.0	418	2	Q7NKE2	Q7NKE2	gloeobacter
998	72	6.0	1275	1	Q9VAE1	Q9VAE1	dirosophila	1071	71.5	6.0	419	2	Q7VAC4	Q7VAC4	prochloroco
999	72	6.0	1282	2	Q24809	Q24809	entamoeba h	1072	71.5	6.0	431	2	Q6BH32	Q6BH32	rattus norv
1000	72	6.0	1477	2	Q9C250	Q9C250	neutrospora	1073	71.5	6.0	435	2	Q8YSE0	Q8YSE0	listeria norv
1001	72	6.0	1513	2	Q7RVU0	Q7RVU0	neutrospora	1074	71.5	6.0	435	2	Q929P5	Q929P5	listeria mo
1002	72	6.0	3010	2	Q9QIX1	Q9QIX1	hepatitis c	1075	71.5	6.0	435	2	Q71XN9	Q71XN9	listeria in
1003	72	6.0	3010	2	Q9QIX2	Q9QIX2	hepatitis c	1076	71.5	6.0	435	2	Q891I7	Q891I7	bradyrhizob
1004	71.5	6.0	161	2	Q88242	Q88242	dennyus som	1077	71.5	6.0	466	2	Q895Q8	Q895Q8	bradyrhizob
1005	71.5	6.0	198	2	Q86X19	Q86X19	homo sapien	1078	71.5	6.0	470	2	Q05351	Q05351	entamoeba h
1006	71.5	6.0	206	2	Q8EYX1	Q8EYX1	leptospiira	1079	71.5	6.0	486	2	Q62XJ5	Q62XJ5	baclillus i1
1007	71.5	6.0	210	2	Q37682	Q37682	typanoplas	1080	71.5	6.0	489	2	Q65M56	Q65M56	baclillus i1
1008	71.5	6.0	225	1	VME1_IBV6	P05136	avian infec	1081	71.5	6.0	501	2	Q9XH61	Q9XH61	matricaria
1009	71.5	6.0	229	2	Q9GAT7	Q9GAT7	avian infec	1082	71.5	6.0	501	2	Q6DB53	Q6DB53	erwinia car
1010	71.5	6.0	229	2	Q7NB29	Q7NB29	mycoplasma	1083	71.5	6.0	518	1	HEX5_RICCO	HEX5_RICCO	ricinus com
1011	71.5	6.0	235	2	Q03191	Q03191	monomortium	1084	71.5	6.0	518	2	Q880G3	Q880G3	pseudomonas
1012	71.5	6.0	237	2	Q06251	Q06251	mycobacteri	1085	71.5	6.0	521	2	Q6CVF0	Q6CVF0	kluyveromyc
1013	71.5	6.0	237	2	Q7TWM5	Q7TWM5	mycobacteri	1086	71.5	6.0	524	2	Q80905	Q80905	arabidopsis
1014	71.5	6.0	246	2	Q8YB21	Q8YB21	brucella me	1087	71.5	6.0	524	2	Q6NH85	Q6NH85	corynebacte
1015	71.5	6.0	254	2	Q8LXQ9	Q8LXQ9	laminaria d	1088	71.5	6.0	536	2	Q81F50	Q81F50	baclillus ce
1016	71.5	6.0	255	2	Q66480	Q66480	equine arte	1089	71.5	6.0	550	2	Q8VMK1	Q8VMK1	pseudomonas
1017	71.5	6.0	257	2	Q71W44	Q71W44	listeria mo	1090	71.5	6.0	550	2	Q881M5	Q881M5	pseudomonas
1018	71.5	6.0	266	2	Q8XP47	Q8XP47	clostridium	1091	71.5	6.0	603	2	Q99R71	Q99R71	staphylococc
1019	71.5	6.0	270	2	Q8H1Y5	Q8H1Y5	perognathus	1092	71.5	6.0	603	2	Q792Y2	Q792Y2	staphylococc
1020	71.5	6.0	301	2	Q9CJ24	Q9CJ24	lactococcus	1093	71.5	6.0	603	2	Q7A3D6	Q7A3D6	staphylococc
1021	71.5	6.0	314	1	OR3_MOUSE	Q8V66	musculus	1094	71.5	6.0	603	2	Q666A7	Q666A7	staphylococc
1022	71.5	6.0	320	2	Q9FAT0	Q9FAT0	vibrio para	1095	71.5	6.0	603	2	Q6GDN2	Q6GDN2	staphylococc
1023	71.5	6.0	326	2	Q7L853	Q7L853	homo sapien	1096	71.5	6.0	651	2	Q9MZX4	Q9MZX4	arabidopsis
1024	71.5	6.0	336	2	Q9BF45	Q9BF45	ceratotheri	1097	71.5	6.0	663	2	Q66HG5	Q66HG5	rattus norv
1025	71.5	6.0	326	2	Q9BF57	Q9BF57	hylobates c	1098	71.5	6.0	669	1	YH06_HABIN	YH06_HABIN	haemophilus
1026	71.5	6.0	328	2	Q89R48	Q89R48	bradyrhizob	1099	71.5	6.0	670	1	SI42_RAT	SI42_RAT	rattus norv
1027	71.5	6.0	332	2	Q8GIP3	Q8GIP3	thermopaga	1100	71.5	6.0	715	2	Q7Z4M8	Q7Z4M8	homo sapien
1028	71.5	6.0	334	2	Q9TZ00	Q9TZ00	caenorhabdi	1101	71.5	6.0	725	1	MTTR_HUMAN	MTTR_HUMAN	homo sapien
1029	71.5	6.0	336	2	Q794Z5	Q794Z5	neomys fodi	1102	71.5	6.0	743	2	Q8GTF2	Q8GTF2	hordium vul
1030	71.5	6.0	336	2	Q9TH84	Q9TH84	sorex radde	1103	71.5	6.0	814	2	Q8D340	Q8D340	caenorhabdi
1031	71.5	6.0	336	2	Q800E8	Q800E8	tetradodon n	1104	71.5	6.0	828	2	Q8D440	Q8D440	vibrio vuln
1032	71.5	6.0	338	2	Q800G2	Q800G2	tetradodon n	1105	71.5	6.0	858	2	Q661Y5	Q661Y5	dictyosteli
1033	71.5	6.0	339	2	Q8RD25	Q8RD25	thermoanaer	1106	71.5	6.0	889	1	WFS1_HUMAN	WFS1_HUMAN	thermoanaer
1034	71.5	6.0	341	2	Q9BRZ1	Q9BRZ1	guillardiia	1107	71.5	6.0	1407	1	CYAA_DICDI	CYAA_DICDI	dictyosteli
1035	71.5	6.0	342	1	V674_HHY8	Q98146	human herpe	1108	71.5	6.0	1509	2	Q6RCS2	Q6RCS2	ciona bavig
1036	71.5	6.0	342	1	Q90387	Q90387	human herpe	1109	71.5	6.0	1837	2	Q6X3J2	Q6X3J2	pseudomonas
1037	71.5	6.0	348	1	RNFD_VIBCH	Q9K189	vibrio chol	1110	71.5	6.0	1923	1	CLR2_HUMAN	CLR2_HUMAN	pyrococcus
1038	71.5	6.0	348	1	Q999Z2	Q999Z2	cyprinella	1111	71.5	6.0	3010	2	Q68949	Q68949	equine arte
1039	71.5	6.0	355	2	Q8YDX2	Q8YDX2	brucella me	1112	71.5	6.0	3589	2	Q6LRF3	Q6LRF3	hepatitis c
1040	71.5	6.0	360	2	Q8H1B6	Q8H1B6	calloscleru	1113	71.5	6.0	5303	2	Q9V6Z8	Q9V6Z8	plasmodium
1041	71.5	6.0	362	2	Q85CY4	Q85CY4	baclillus i1	1114	71.5	5.9	114	2	Q25269	Q25269	helicobacte
1042	71.5	6.0	362	1	Q6PDP2	Q6PDP2	mus muscullu	1115	71.5	5.9	150	2	Q82ZC0	Q82ZC0	enterococcu
1043	71.5	6.0	366	1	MLIA_SHEEP	P48040	cvis aries	1116	71.5	5.9	171	2	Q8UJQ3	Q8UJQ3	pyrococcus
1044	71.5	6.0	369	2	Q70VH8	Q70VH8	sorex minut	1117	71.5	5.9	173	2	Q9WD21	Q9WD21	equine arte
1045	71.5	6.0	375	2	Q6RKP7	Q6RKP7	human herpe	1118	71.5	5.9	188	1	5H2A_CANFA	5H2A_CANFA	canis famli
1046	71.5	6.0	379	1	CYB_OCHCO	Q953J5	ochotona co	1119	71.5	5.9	195	2	Q6MTK4	Q6MTK4	mycoplasma
1047	71.5	6.0	379	1	CYB_OCHFO	Q9B4Y5	ochotona fo	1120	71.5	5.9	199	2	Q8TMM3	Q8TMM3	methanosarc
1048	71.5	6.0	379	1	CYB_SORR4	Q79462	sorex radde	1121	71.5	5.9	200	2	Q85U08	Q85U08	ceratobaeus
1049	71.5	6.0	379	1	CYB_SPEPA	Q9TF55	spermophilu	1122	71.5	5.9	200	2	Q9J7J9	Q9J7J9	starchine rep
1050	71.5	6.0	379	2	Q48007	Q48007	perognathus	1123	71.5	5.9	219	2	Q93JID2	Q93JID2	pyrobaculum
1051	71.5	6.0	379	2	Q8MEK3	Q8MEK3	thomomys ta	1124	71.5	5.9	223	2	Q91NKS	Q91NKS	avian infec
1052	71.5	6.0	379	2	Q952R3	Q952R3	glaucomys b	1125	71.5	5.9	223	2	Q91NKS	Q91NKS	avian infec
1053	71.5	6.0	379	2	Q34661	Q34661	glaucomys b	1126	71.5	5.9	223	2	Q91S95	Q91S95	avian infec

1127	71	5.9	223	2	091596	091596 avian infec	1200	71	5.9	470	1	5H2A_PIG	P50129 sus scrofa
1128	71	5.9	223	1	0915A3	0915A3 avian infec	1201	71	5.9	471	1	5H2A_HUMAN	P28223 homo sapien
1129	71	5.9	225	1	0915A3	P12649 avian infec	1202	71	5.9	472	2	06K136	06K136 mycoplasma
1130	71	5.9	225	2	06R4P1	06R4P1 avian infec	1203	71	5.9	480	2	073CA7	073CA7 bacillus ce
1131	71	5.9	225	2	07TEG9	07TEG9 avian infec	1204	71	5.9	485	2	09CLJ7	09CLJ7 pasteurella
1132	71	5.9	226	2	07T405	07T405 avian infec	1205	71	5.9	489	2	08SHRO	08SHRO trichoderma
1133	71	5.9	234	2	09F6V0	09F6V0 bacteroides	1206	71	5.9	492	2	07N9D9	07N9D9 photorhabdu
1134	71	5.9	238	1	09F6V0	09F6V0 bacteroides	1207	71	5.9	545	1	SOA1_RAT	070556 ratus norv
1135	71	5.9	238	2	09T4G5	09T4G5 phlebotomus	1208	71	5.9	546	1	MUP3_YEAST	P38734 saccharomyc
1136	71	5.9	238	2	09T4G5	09T4G5 phlebotomus	1209	71	5.9	546	1	0813H5	0813H5 phlebotomus
1137	71	5.9	238	2	09T4G5	09T4G5 phlebotomus	1210	71	5.9	554	2	08AUN9	08AUN9 fugu rubrip
1138	71	5.9	238	2	09T4G5	09T4G5 phlebotomus	1211	71	5.9	554	2	YAS8_SCHPO	Q10144 schizosacch
1139	71	5.9	242	2	0639U8	0639U8 bacillus ce	1212	71	5.9	563	1	S229_MOUSE	09wtc6 mus musculu
1140	71	5.9	243	2	034969	034969 myrmecia ba	1213	71	5.9	564	1	06F1V1	06F1V1 mesoplasma
1141	71	5.9	244	2	074HS0	074HS0 lactobacilli	1214	71	5.9	576	1	OCCT1_CABEL	09U539 caenorhabdi
1142	71	5.9	250	2	09KVO3	09KVO3 vibrio chol	1215	71	5.9	584	1	LYTS_STRAU	053705 staphylococ
1143	71	5.9	255	2	066484	066484 equine arte	1216	71	5.9	615	2	07R9S0	07R9S0 plasmodium
1144	71	5.9	258	2	09PP98	09PP98 campylobact	1217	71	5.9	620	2	092ZP7	092ZP7 cyanidlovch
1145	71	5.9	266	2	06W249	06W249 rhizobium s	1218	71	5.9	631	2	081W20	081W20 homo sapien
1146	71	5.9	277	2	070NM1	070NM1 strongyloid	1219	71	5.9	672	2	0650E2	0650E2 bacteroides
1147	71	5.9	279	2	07NEM0	07NEM0 mycoplasma	1220	71	5.9	676	2	004521	004521 arabisdopsis
1148	71	5.9	281	2	08SK19	08SK19 necator ame	1221	71	5.9	701	2	08EWU9	08EWU9 mycoplasma
1149	71	5.9	286	2	063CT1	063CT1 bacillus ce	1222	71	5.9	762	2	08ML23	08ML23 drosophila
1150	71	5.9	289	2	08HZF2	08HZF2 macaca sp.	1223	71	5.9	788	2	092JYB7	092JYB7 helicobacte
1151	71	5.9	290	2	084A_ARATH	084A_ARATH arabisdopsis	1224	71	5.9	826	2	08TOX6	08TOX6 methanobarc
1152	71	5.9	295	2	08P0V2	08P0V2 streptococc	1225	71	5.9	885	2	075BR1	075BR1 ashbya gos
1153	71	5.9	295	2	09ZG23	09ZG23 streptococc	1226	71	5.9	913	2	013099	013099 xenopus lae
1154	71	5.9	295	2	07CNV1	07CNV1 streptococc	1227	71	5.9	913	2	06DC00	06DC00 xenopus lae
1155	71	5.9	308	1	SRV1_CABEL	SRV1_CABEL caenorhabdi	1228	71	5.9	964	2	07SCL0	07SCL0 neurospora
1156	71	5.9	310	1	Y160_BUCAP	Y160_BUCAP buchnera ap	1229	71	5.9	1021	2	065QR6	065QR6 manihelma
1157	71	5.9	335	2	099NR9	099NR9 tamias atri	1230	71	5.9	1239	2	06CBA1	06CBA1 yarrowia li
1158	71	5.9	343	2	07YFU4	07YFU4 myrmica kar	1231	71	5.9	1242	2	07T9B1	07T9B1 human cytom
1159	71	5.9	345	2	078911	078911 anolis occu	1232	71	5.9	1409	2	07XW92	07XW92 cryza sattiv
1160	71	5.9	361	2	098P01	098P01 mycoplasma	1233	71	5.9	2304	2	09BMQ4	09BMQ4 lactella g
1161	71	5.9	374	2	071EAS	071EAS galierella s	1234	71	5.9	2433	2	077393	077393 plasmodium
1162	71	5.9	379	1	CYB_CRATY	08Wd1 cratogeomys	1235	71	5.9	2681	2	095V80	095V80 strongyloce
1163	71	5.9	379	1	CYB_THOUM	047993 thomomys um	1236	71	5.9	3010	2	06B285	06B285 hepatitis c
1164	71	5.9	379	2	047579	047979 thomomys bo	1237	71	5.9	3010	2	081541	081541 hepatitis c
1165	71	5.9	379	2	047981	047981 thomomys bo	1238	71	5.9	3010	2	081825	081825 hepatitis c
1166	71	5.9	379	2	08W7H1	08W7H1 thomomys ma	1239	71	5.9	3010	2	09D7B5	09D7B5 hepatitis c
1167	71	5.9	379	2	0698P7	0698P7 cratogeomys	1240	71	5.9	145	2	065G39	065G39 bacillus li
1168	71	5.9	379	2	0698P9	0698P9 cratogeomys	1241	71	5.9	203	1	BCRC_BACLI	P42334 bacillus li
1169	71	5.9	379	2	06OK63	06OK63 ursus thibe	1242	71	5.9	206	2	072LX2	072LX2 leprospira
1170	71	5.9	379	2	09TF00	09TF00 geomys bure	1243	71	5.9	208	2	06BHB0	06BHB0 debraryomyc
1171	71	5.9	379	2	09TF03	09TF03 geomys bure	1244	71	5.9	213	2	098E85	098E85 rhizobium l
1172	71	5.9	380	2	003396	003397 acomys sp.	1245	71	5.9	214	2	06VRP1	06VRP1 dipodomys o
1173	71	5.9	380	2	003397	003397 acomys sp.	1246	71	5.9	216	2	06VRP1	06VRP1 dipodomys o
1174	71	5.9	380	2	06E3J7	06E3J7 thomomys bo	1247	71	5.9	226	2	003371	003371 dipodomys o
1175	71	5.9	380	2	09T502	09T502 geomys brev	1248	71	5.9	235	2	06BAU8	06BAU8 ovis aries
1176	71	5.9	380	2	09T576	09T576 acomys sp.	1249	71	5.9	235	2	06DHQ1	06DHQ1 schizosacch
1177	71	5.9	380	2	09T577	09T577 acomys sp.	1250	71	5.9	266	2	074888	074888 agrobacteri
1178	71	5.9	380	2	08EM01	08EM01 oceanobacill	1251	71	5.9	266	2	08U854	08U854 agrobacteri
1179	71	5.9	381	1	CYB_PHACT	035409 phascogalea	1252	71	5.9	278	2	08SHQ3	08SHQ3 cooperia on
1180	71	5.9	391	2	08RLY8	08RLY8 salmonella	1253	71	5.9	279	2	08YVW2	08YVW2 anabaena sp
1181	71	5.9	391	2	08RSP4	08RSP4 salmonella	1254	71	5.9	283	2	09AKZ0	09AKZ0 lacobacilli
1182	71	5.9	391	2	09CUI8	09CUI8 lactococcus	1255	71	5.9	285	2	07S2B8	07S2B8 neurospora
1183	71	5.9	401	2	0850S5	0850S5 cryza sattiv	1256	71	5.9	280	2	06SCH2	06SCH2 uncultured
1184	71	5.9	403	2	08ZPR2	08ZPR2 salmonella	1257	71	5.9	291	2	037789	037789 hellanthus
1185	71	5.9	409	2	09F2J6	09F2J6 streptomyc	1258	71	5.9	292	2	0746W1	0746W1 geobacter s
1186	71	5.9	416	2	09AB3C	09AB3C caulobacter	1259	71	5.9	310	2	065VD8	065VD8 manihelma li
1187	71	5.9	418	2	06OPF6	06OPF6 legionella	1260	71	5.9	312	2	06CEC0	06CEC0 yarrowia li
1188	71	5.9	418	2	06OPF0	06OPF0 legionella	1261	71	5.9	315	2	09JRK5	09JRK5 ratus norv
1189	71	5.9	418	2	06OPF0	06OPF0 legionella	1262	71	5.9	320	2	07N0S0	07N0S0 photorhabdu
1190	71	5.9	418	2	06OPF2	06OPF2 legionella	1263	71	5.9	326	2	09BR39	09BR39 mania penta
1191	71	5.9	418	2	06OPF4	06OPF4 legionella	1264	71	5.9	326	2	09BR58	09BR58 macaca mula
1192	71	5.9	418	2	06OPF6	06OPF6 legionella	1265	71	5.9	335	2	09ZV31	09ZV31 elephanticu
1193	71	5.9	419	2	095081	095081 caenorhabdi	1266	71	5.9	336	2	09THB3	09THB3 sorex pacific
1194	71	5.9	423	2	08Y5H6	08Y5H6 listeria mo	1267	71	5.9	339	2	07PB28	07PB28 rickettsia
1195	71	5.9	438	2	0615Y4	0615Y4 cryza sattiv	1268	71	5.9	340	2	055632	055632 synchocyst
1196	71	5.9	442	2	096ZK3	096ZK3 sulfolobus	1269	71	5.9	343	2	07Y7B1	07Y7B1 myrmica nit
1197	71	5.9	448	2	0916B3	0916B3 diptophila	1270	71	5.9	343	2	07Y7B5	07Y7B5 myrmica sab
1198	71	5.9	451	2	09SNW3	09SNW3 vernicia fo	1271	71	5.9	343	2	07YFUS	07YFUS myrmica hel
1199	71	5.9	451	2	09F992	09F992 buchnera ap	1272	71	5.9	350	2	09Y370	09Y370 homo sapien

1273	70.5	5.9	351	2	Q97774	Q97774 felis silve	1346	70.5	5.9	676	2	Q7RNV6	Q7RNV6 plasmodium
1274	70.5	5.9	352	2	Q9BR08	Q9BR08 mycoplasma	1347	70.5	5.9	679	2	Q7Q645	Q7Q645 anopheles g
1275	70.5	5.9	353	2	Q7TN44	Q7TN44 rattus norv	1348	70.5	5.9	683	2	Q972H7	Q972H7 sulfobius
1276	70.5	5.9	356	2	Q9GCR9	Q9GCR9 glaucomyx v	1349	70.5	5.9	689	2	Q7ZYU0	Q7ZYU0 bacillus ce
1277	70.5	5.9	360	2	Q9HC18	Q9HC18 calloscleru	1350	70.5	5.9	700	2	Q9LDT0	Q9LDT0 arabisopsis
1278	70.5	5.9	360	2	Q9HC13	Q9HC13 calloscleru	1351	70.5	5.9	717	2	Q6NHL8	Q6NHL8 cornebacte
1279	70.5	5.9	361	2	Q9N4V8	Q9N4V8 caenorhabd	1352	70.5	5.9	729	2	Q9ESC5	Q9ESC5 oceanobacil
1280	70.5	5.9	363	2	Q9K337	Q9K337 bacillus ce	1353	70.5	5.9	740	2	Q9XCM9	Q9XCM9 oryza sativ
1281	70.5	5.9	363	2	Q9K337	Q9K337 bacillus ce	1354	70.5	5.9	740	2	Q9FRK0	Q9FRK0 oryza sativ
1282	70.5	5.9	366	2	Q6TTY3	Q6TTY3 homo sapien	1355	70.5	5.9	766	2	Q9LZ30	Q9LZ30 arabisopsis
1283	70.5	5.9	369	2	Q70VB2	Q70VB2 seorex volu	1356	70.5	5.9	769	2	Q7W1T5	Q7W1T5 bordetella
1284	70.5	5.9	370	2	Q6VPS4	Q6VPS4 canis famil	1357	70.5	5.9	776	1	CHS1_CANAL	B2336 candida alb
1285	70.5	5.9	370	2	Q7RFS0	Q7RFS0 plasmodium	1358	70.5	5.9	856	2	Q9FHV2	Q9FHV2 arabisopsis
1286	70.5	5.9	373	2	Q6UTJ34	Q6UTJ34 heptathela	1359	70.5	5.9	899	2	Q9FPI4	Q9FPI4 candida gla
1287	70.5	5.9	379	1	CYB_GIAV0	Q9CF34 glaucomyx v	1360	70.5	5.9	951	2	Q6PK21	Q6PK21 bacteroides
1288	70.5	5.9	379	2	Q48009	Q48009 dipodomys a	1361	70.5	5.9	980	2	Q9A3J1	Q9A3J1 candida alb
1289	70.5	5.9	379	2	Q48354	Q48354 thomomys bo	1362	70.5	5.9	1026	2	Q9URM1	Q9URM1 candida alb
1290	70.5	5.9	379	2	Q8LW04	Q8LW04 macroscelid	1363	70.5	5.9	1199	2	Q9Y4J9	Q9Y4J9 homo sapien
1291	70.5	5.9	379	2	Q8W9L6	Q8W9L6 glaucomyx v	1364	70.5	5.9	1234	2	Q8VDJ4	Q8VDJ4 mus musculu
1292	70.5	5.9	379	2	Q85RV3	Q85RV3 muntiacus c	1365	70.5	5.9	1234	2	Q6B4R6	Q6B4R6 mus musculu
1293	70.5	5.9	379	2	Q9GAV5	Q9GAV5 dipodomys v	1366	70.5	5.9	1491	2	Q7S5P1	Q7S5P1 neurospora
1294	70.5	5.9	379	2	Q9GAV6	Q9GAV6 dipodomys v	1367	70.5	5.9	1583	2	Q92GE9	Q92GE9 rickettsia
1295	70.5	5.9	379	2	Q9GAV7	Q9GAV7 dipodomys o	1368	70.5	5.9	1678	2	Q6BD82	Q6BD82 homo sapien
1296	70.5	5.9	379	2	Q9GAV9	Q9GAV9 dipodomys e	1369	70.5	5.9	1764	2	Q8BRJ3	Q8BRJ3 strongyloce
1297	70.5	5.9	379	2	Q9GAN1	Q9GAN1 dipodomys e	1370	70.5	5.9	1781	1	AKI2_HUMAN	Q02932 homo sapien
1298	70.5	5.9	379	2	Q9GAN5	Q9GAN5 dipodomys e	1371	70.5	5.9	1787	1	CHD3_CAEEL	Q22516 caenorhabd
1299	70.5	5.9	379	2	Q9GBY3	Q9GBY3 ochotona da	1372	70.5	5.9	5138	2	Q9ZW94	Q9ZW94 arabisopsis
1300	70.5	5.9	379	2	Q9TEZ7	Q9TEZ7 geomys burs	1373	70.5	5.9	80	2	Q7N019	Q7N019 photorhabdu
1301	70.5	5.9	382	2	Q9H1E9	Q9H1E9 thermoplasm	1374	70.5	5.9	114	2	Q6VRH8	Q6VRH8 helicobacte
1302	70.5	5.9	386	2	Q6RKP3	Q6RKP3 human herpe	1375	70.5	5.9	114	2	Q6VRL8	Q6VRL8 helicobacte
1303	70.5	5.9	387	1	T2C_PARTIE	Q27181 paramecium	1376	70.5	5.9	146	2	Q8T098	Q8T098 drosoephila
1304	70.5	5.9	389	1	MTR_BUFA	Q90252 bufu marinu	1377	70.5	5.9	154	1	ML1A_PIG	Q02781 sus scrofa
1305	70.5	5.9	390	1	PEZ3_HUMAN	P3115 homo sapien	1378	70.5	5.9	161	2	Q65J32	Q65J32 bacillus li
1306	70.5	5.9	393	2	Q00326	Q00326 homo sapien	1379	70.5	5.9	173	2	Q67EWS	Q67EWS equine arte
1307	70.5	5.9	394	2	Q8X1V7	Q8X1V7 coriolus ve	1380	70.5	5.9	173	2	Q9WD20	Q9WD20 equine arte
1308	70.5	5.9	402	2	Q00325	Q00325 homo sapien	1381	70.5	5.9	173	2	Q9WD23	Q9WD23 equine arte
1309	70.5	5.9	403	2	Q9KGT1	Q9KGT1 mycoplasma	1382	70.5	5.9	173	2	Q9WD35	Q9WD35 equine arte
1310	70.5	5.9	414	2	Q6Z9G4	Q6Z9G4 oryza sativ	1383	70.5	5.9	175	2	Q9HL28	Q9HL28 thermoplasm
1311	70.5	5.9	416	2	Q6VPS5	Q6VPS5 canis famil	1384	70.5	5.9	185	2	Q9HL28	Q9HL28 arabisopsis
1312	70.5	5.9	420	2	Q7BR79	Q7BR79 aeromonas p	1385	70.5	5.9	189	1	PSBY_ARATH	Q49347 arabisopsis
1313	70.5	5.9	423	2	Q58964	Q58964 pyrococcus	1386	70.5	5.9	195	2	Q86RF5	Q86RF5 schistosoma
1314	70.5	5.9	424	2	Q7VP09	Q7VP09 helicobacte	1387	70.5	5.9	195	2	Q85QZ5	Q85QZ5 lepus europ
1315	70.5	5.9	436	2	Q6BUT5	Q6BUT5 debaryomyce	1388	70.5	5.9	199	1	PSBY_ARATH	Q84710 spiraciola ol
1316	70.5	5.9	440	1	CAPE_STRAU	P39854 staphylococ	1389	70.5	5.9	213	2	Q9LNR6	Q9LNR6 arabisopsis
1317	70.5	5.9	452	2	Q83C47	Q83C47 coxiella bu	1390	70.5	5.9	221	2	Q9B9P3	Q9B9P3 viverra zib
1318	70.5	5.9	460	2	Q7VIR8	Q7VIR8 helicobacte	1391	70.5	5.9	223	2	Q9INK4	Q9INK4 avian infec
1319	70.5	5.9	470	2	Q6SED7	Q6SED7 lactobacill	1392	70.5	5.9	224	2	Q8VSW5	Q8VSW5 staphylococ
1320	70.5	5.9	470	2	Q6SPD0	Q6SPD0 lactobacill	1393	70.5	5.9	225	1	VMEL_IBVD1	Q91486 avian infec
1321	70.5	5.9	472	2	Q9LNC5	Q9LNC5 microtomosp	1394	70.5	5.9	225	1	VMEL_IBVD1	Q91486 avian infec
1322	70.5	5.9	472	2	Q8YCO7	Q8YCO7 bruceella me	1395	70.5	5.9	225	2	VMEL_IBVM	Q91987 avian infec
1323	70.5	5.9	496	2	Q25600	Q25600 helicobacte	1396	70.5	5.9	225	2	Q6VUR1	Q6VUR1 avian infec
1324	70.5	5.9	496	2	Q8EC04	Q8EC04 staphylococ	1397	70.5	5.9	225	2	Q6W9D6	Q6W9D6 avian infec
1325	70.5	5.9	500	2	Q8EC01	Q8EC01 oceanobacil	1398	70.5	5.9	225	2	Q7TEH1	Q7TEH1 avian infec
1326	70.5	5.9	508	2	Q7RQY6	Q7RQY6 plasmodium	1399	70.5	5.9	225	2	Q8RTB1	Q8RTB1 fusobacteri
1327	70.5	5.9	521	1	CYOA_HABIN	P45021 haemophilus	1400	70.5	5.9	236	2	Q9XMR1	Q9XMR1 phlebotomus
1328	70.5	5.9	536	1	WVIN_CHLMU	Q9PJ09 chlamydia m	1401	70.5	5.9	238	2	Q9XMR1	Q9XMR1 phlebotomus
1329	70.5	5.9	556	2	Q22109	Q22109 caenorhabd	1402	70.5	5.9	249	2	Q6T2A1	Q6T2A1 polythachis
1330	70.5	5.9	556	2	Q7VH12	Q7VH12 helicobacte	1403	70.5	5.9	253	2	Q7NTR1	Q7NTR1 chromobact
1331	70.5	5.9	558	2	Q6E1C5	Q6E1C5 perkinsus m	1404	70.5	5.9	255	2	Q995W3	Q995W3 equine arte
1332	70.5	5.9	574	1	RFT1_YEAST	P38206 baccharomyc	1405	70.5	5.9	255	2	Q9QKE1	Q9QKE1 equine arte
1333	70.5	5.9	585	2	Q7R1V4	Q7R1V4 giardia lam	1406	70.5	5.9	256	2	Q76B99	Q76B99 dirosophila
1334	70.5	5.9	598	1	S6A1_MOUSE	P41648 mus cookii	1407	70.5	5.9	257	2	Q65V41	Q65V41 manhelina
1335	70.5	5.9	599	1	S6A1_MOUSE	P31648 mus musculu	1408	70.5	5.9	257	2	Q876G0	Q876G0 saccharomyc
1336	70.5	5.9	599	1	S6A1_MOUSE	P31648 mus musculu	1409	70.5	5.9	281	2	Q70Q29	Q70Q29 necator ame
1337	70.5	5.9	599	1	S6A1_MOUSE	P31648 mus musculu	1410	70.5	5.9	287	1	CB4B_ARATH	Q9XF88 arabisopsis
1338	70.5	5.9	633	2	Q7Q802	Q7Q802 giardia lam	1411	70.5	5.9	289	2	Q8H2F4	Q8H2F4 gorilla gor
1339	70.5	5.9	641	2	Q7PMH7	Q7PMH7 anopheles g	1412	70.5	5.9	289	2	Q8H2F5	Q8H2F5 pan troglod
1340	70.5	5.9	658	2	Q7ZUP5	Q7ZUP5 brachydanio	1413	70.5	5.9	289	2	Q7NIV8	Q7NIV8 gloeobacter
1341	70.5	5.9	662	1	T9S2_MOUSE	P58021 mus musculu	1414	70.5	5.9	292	1	ATP6_MYCG	P47645 mycoplasma
1342	70.5	5.9	662	1	T9S2_MOUSE	P58021 mus musculu	1415	70.5	5.9	292	2	Q92KZ8	Q92KZ8 rhizobium m
1343	70.5	5.9	662	2	Q8CFP9	Q8CFP9 mus musculu	1416	70.5	5.9	295	2	Q65UR1	Q65UR1 manhelina
1344	70.5	5.9	667	2	Q9G654	Q9G654 malawimonas	1417	70.5	5.9	299	2	Q6MCO9	Q6MCO9 methanococ
1345	70.5	5.9	676	2	Q7Q114	Q7Q114 anopheles g	1418	70.5	5.9	302	2	Q9M7X8	Q9M7X8 arabisopsis

1419	70	5.9	303	2	08KJ79	08KJ79 rhizobium 1
1420	70	5.9	305	2	087R04	087R04 vibrio para
1421	70	5.9	307	2	097T64	097T64 streptococ
1422	70	5.9	307	2	08DRJ7	08DRJ7 streptococ
1423	70	5.9	308	2	06FSR9	06FSR9 candida gla
1424	70	5.9	311	2	09JHE2	09JHE2 rattus norv
1425	70	5.9	325	2	09G3Z5	09G3Z5 lithobius f
1426	70	5.9	328	2	08D0N5	08D0N5 yerarsinia p
1427	70	5.9	330	2	094303	094303 caenorhabd
1428	70	5.9	332	2	08SEB3	08SEB3 mtu tubero
1429	70	5.9	333	1	06R8_HUMAN	06R8_HUMAN
1430	70	5.9	333	2	06NMQ5	06NMQ5 homo sapien
1431	70	5.9	333	2	06NMQ6	06NMQ6 homo sapien
1432	70	5.9	345	2	06X0B8	06X0B8 anolis whit
1433	70	5.9	345	2	06X0C1	06X0C1 anolis whit
1434	70	5.9	345	2	06X0C4	06X0C4 anolis whit
1435	70	5.9	353	2	08TNU4	08TNU4 methanocarc
1436	70	5.9	353	2	08TNU4	08TNU4 methanocarc
1437	70	5.9	365	2	09XMT1	09XMT1 tetrahymena
1438	70	5.9	365	2	06A7G0	06A7G0 propionibac
1439	70	5.9	371	2	09NT82	09NT82 homo sapien
1440	70	5.9	378	2	06UVN5	06UVN5 toxodonta c
1441	70	5.9	378	2	071FH4	071FH4 toxodonta c
1442	70	5.9	379	1	CYB_SORTU	CYB_SORTU
1443	70	5.9	379	1	CYB_ZIPCA	CYB_ZIPCA
1444	70	5.9	379	2	047578	047578 thomomys bo
1445	70	5.9	379	2	047583	047583 thomomys bo
1446	70	5.9	379	2	047994	047994 thomomys um
1447	70	5.9	379	2	08LVE7	08LVE7 proteles cr
1448	70	5.9	379	2	08LMD6	08LMD6 parahaena
1449	70	5.9	379	2	08W935	08W935 thomomys ma
1450	70	5.9	379	2	08WDU4	08WDU4 cratogeomys
1451	70	5.9	379	2	08WEK4	08WEK4 thomomys ta
1452	70	5.9	379	2	034837	034837 kogia salms
1453	70	5.9	379	2	06T1B4	06T1B4 kogia texe
1454	70	5.9	379	2	071FH8	071FH8 nandinia bl
1455	70	5.9	379	2	07Y8J5	07Y8J5 procavia ca
1456	70	5.9	379	2	08HB13	08HB13 thomomys bo
1457	70	5.9	379	2	08HB6C	08HB6C thomomys bo
1458	70	5.9	379	2	08HB83	08HB83 thomomys bo
1459	70	5.9	379	2	08HBK4	08HBK4 thomomys bo
1460	70	5.9	379	2	08HHJ3	08HHJ3 thomomys bo
1461	70	5.9	379	2	08HHJ5	08HHJ5 thomomys bo
1462	70	5.9	379	2	08HHJ6	08HHJ6 thomomys bo
1463	70	5.9	379	2	08HHJ8	08HHJ8 thomomys bo
1464	70	5.9	380	2	06E3J6	06E3J6 thomomys bo
1465	70	5.9	381	1	CYB_DASAL	CYB_DASAL
1466	70	5.9	381	1	CYB_DASNA	CYB_DASNA
1467	70	5.9	381	1	CYB_DASSP	CYB_DASSP
1468	70	5.9	381	1	CYB_DASVI	CYB_DASVI
1469	70	5.9	381	1	CYB_MYOME	CYB_MYOME
1470	70	5.9	381	1	CYB_MYOMA	CYB_MYOMA
1471	70	5.9	388	1	OXYR_MOUSE	OXYR_MOUSE
1472	70	5.9	388	1	OXYR_RAT	OXYR_RAT
1473	70	5.9	388	2	08R5E1	08R5E1 rattus norv
1474	70	5.9	399	2	096A40	096A40 homo sapien
1475	70	5.9	399	2	08MID0	08MID0 manis tatra
1476	70	5.9	407	2	086894	086894 streptococ
1477	70	5.9	407	2	09RIN7	09RIN7 streptococ
1478	70	5.9	416	2	09MON4	09MON4 arabiidops
1479	70	5.9	418	2	054543	054543 legionella
1480	70	5.9	418	2	06QFB3	06QFB3 legionella
1481	70	5.9	420	2	09WZ65	09WZ65 thermocoga
1482	70	5.9	420	2	082490	082490 arabiidops
1483	70	5.9	427	2	06MDN6	06MDN6 parachlamyd
1484	70	5.9	427	2	08X581	08X581 escherichia
1485	70	5.9	437	2	08FAY1	08FAY1 escherichia
1486	70	5.9	437	2	083P88	083P88 shigella fl
1487	70	5.9	438	2	08UDM3	08UDM3 agrobacteri
1488	70	5.9	450	2	039292	039292 equid herpe
1489	70	5.9	452	2	07RNL9	07RNL9 plasmodium
1490	70	5.9	461	2	07N4W5	07N4W5 photorhabdu
1491	70	5.9	467	2	06C7W7	06C7W7 yarrowia ll

1492	70	5.9	467	2	08MPH2	08MPH2 trypanosoma
1493	70	5.9	476	2	06A0F5	06A0F5 desulfocale
1494	70	5.9	479	2	087J34	087J34 vibrio chol
1495	70	5.9	494	2	023508	023508 caenorhabd1
1496	70	5.9	494	2	08NXX6	08NXX6 staphylococ
1497	70	5.9	494	2	099W27	099W27 staphylococ
1498	70	5.9	494	2	07A762	07A762 staphylococ
1499	70	5.9	494	2	06GBQ3	06GBQ3 staphylococ
1500	70	5.9	494	2	06G3B5	06G3B5 staphylococ

ALIGNMENTS					
RESULT 1	MENT_HUMAN	STANDARD;	PRT;	234 AA.	
AC	095772;				
DT	28-FEB-2003 (Rel. 41, Created)				
DT	28-FEB-2003 (Rel. 41, Last sequence update)				
DT	05-JUL-2004 (Rel. 44, Last annotation update)				
DE	MLN64 N-terminal domain homolog (STARD3 N-terminal like protein) (UNQ855/BRO1864).				
GN	Name=STARD3NL; Synonyms=MENTHO;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A., CHARACTERIZATION, TOPOLOGY, PHOSPHORYLATION, AND				
RP	ALTERNATIVE INITIATION.				
RC	TISSUE=Fetal brain;				
RX	MEDLINE=22384343; PubMed=123393907; DOI=10.1074/jbc.M208290200;				
RT	Alpy F., Wendling C., Rio M.-C., Tomasetto C.;				
RL	"MENTHO, a MLN64 homologue devoid of the START domain.";				
RN	J. Biol. Chem. 277:50780-50787(2002).				
RN	[2]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=22867236; PubMed=12975309; DOI=10.1101/gr.1293003;				
RA	Clark H.F., Gurney A.L., Abaya E., Baker K., Baldwin D., Brush J.,				
RA	Eaton J., Chow B., Chui C., Crowley C., Currell B., Deuel B., Dowd P.,				
RA	Baton D., Foster J., Grimaldi C., Gu Q., Hase P.B., Heldens S.,				
RA	Huang A., Kim H.S., Klimowski L., Jin Y., Johnson S., Lee J.,				
RA	Lewis L., Liao D., Mark M., Robbie E., Sanchez C., Schoenfeld J.,				
RA	Sehagiri S., Simmons L., Singh J., Smith V., Stinson J., Vagstad A.,				
RA	Vandlen R., Watanabe C., Wleand D., Woods K., Xie M.-H., Yansura D.,				
RA	Yi S., Yu G., Yuan J., Zhang M., Zhang Z., Goddard A., Wood W.I.,				
RA	Godowski P., Gray A.;				
RT	"The secreted protein discovery initiative (SPDI), a large-scale				
RT	effort to identify novel human secreted and transmembrane proteins: a				
RT	bioinformatics assessment.";				
RL	Genome Res. 13:2265-2270(2003).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RA	Arnett C., Wohldmann P., Le T.;				
RL	Submitted (FEB-1999) to the EMBL/GenBank/DBJ databases.				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RC	TISSUE=Brain, and Kidney;				
RX	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;				
RA	Straussberg R.L., Feingold E.A., Grouse L.H., Derje J.G.,				
RA	Klausner R.D., Collins F.S., Wagner L., Siemen C.M., Schuler G.D.,				
RA	Altshul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,				
RA	Hopkins R.F., Jordan H., Moore T., Max S.T., Wang J., Hsieh F.,				
RA	Diatcenko L., Marusik A.K., Farmer A.A., Rubin G.M., Hong L.,				
RA	Scapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,				
RA	Brownstein M.J., Udell T.B., Tothiyuki S., Casanovi P., Mullaby S.J.,				
RA	Raha S.S., Loggiano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,				
RA	Bohak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gutierrez P.H.,				
RA	Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huiy S.W.,				
RA	Villalona D.K., Muzny D.C., Hale S., Garcia A.M., Gay L.V., Huiy S.W.,				
RA	Pahey J., Halton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,				
RA	Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,				

RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
 CC membrane protein.
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative initiation;
 CC Comment=2 isoforms, 1 (shown here) and 2, are produced by
 CC alternative initiation;
 CC -1- PTM: Phosphorylated.
 CC -1- SIMILARITY: Contains 1 MENTAL domain.
 CC -----
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 DR EMBL; AJ492267; CAD37353.1; -
 DR EMBL; AY358645; AA089008.1; -
 DR EMBL; AC006033; AA07552.1; -
 DR EMBL; BC003074; AA03074.1; -
 DR EMBL; BC005959; AA05959.1; -
 DR Genew; HGNC:19169; STAND3NL.
 KW Alternative initiation; Phosphorylation; Transmembrane.
 FT CHAIN 1 234
 FT M1N64 N-terminal domain homolog, isoform
 FT 1.
 FT CHAIN 2 234
 FT M1N64 N-terminal domain homolog, isoform
 FT 2.
 FT INIT MET 8 234
 FT DOMAIN 48 218
 FT TRANSMEM 1 53
 FT DOMAIN 54 74
 FT TRANSMEM 75 97
 FT TRANSMEM 98 118
 FT DOMAIN 119 122
 FT TRANSMEM 123 143
 FT DOMAIN 144 150
 FT TRANSMEM 151 171
 FT DOMAIN 172 234
 SQ SEQUENCE 234 AA; 26654 MW; AFB7DAE381983FB0 CRC64;

Query Match 100.0%; Score 1195; DB 1; Length 234;
 Best Local Similarity 100.0%; Pred. NO. 3.3e-100;
 Matches 234; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNHLPEBMEKNTLSSQSHSLRNHINPQLMARIESYGRKKGISDVRFFCFEYV 60
 DB 1 MNHLPEBMEKNTLSSQSHSLRNHINPQLMARIESYGRKKGISDVRFFCFEYV 60
 QY 61 FDLLEFVTLMTIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVFRFKVLLAVAVCRL 120
 DB 61 FDLLEFVTLMTIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVFRFKVLLAVAVCRL 120
 QY 61 FDLLEFVTLMTIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVFRFKVLLAVAVCRL 120
 DB 61 FDLLEFVTLMTIELNVNGGIENTLEKEVMQDYSSYFDIFLLAVFRFKVLLAVAVCRL 120
 QY 121 RHHWMAIALTTAVTSAPFLAKYISKLTFSQCAFVGLPLIISITLAMIETWELDFVLPQEA 180
 DB 121 RHHWMAIALTTAVTSAPFLAKYISKLTFSQCAFVGLPLIISITLAMIETWELDFVLPQEA 180
 QY 121 RHHWMAIALTTAVTSAPFLAKYISKLTFSQCAFVGLPLIISITLAMIETWELDFVLPQEA 180
 DB 121 RHHWMAIALTTAVTSAPFLAKYISKLTFSQCAFVGLPLIISITLAMIETWELDFVLPQEA 180
 QY 181 EENRRLIIVDASRRALIPGSGSDQFYSPSESEASEEKEKODESKPLLEL 234
 DB 181 EENRRLIIVDASRRALIPGSGSDQFYSPSESEASEEKEKODESKPLLEL 234

RESULT 2
 MENT_MOUSE STANDARD; PRT; 235 AA.
 ID Q9DCI3; Q9J463; Q9J356;

DT 28-FEB-2003 (Rel. 41, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUN-2004 (Rel. 44, Last annotation update)
 DE M1N64 N-terminal domain homolog (STARD3 N-terminal like protein).
 GN Name=stard3l; Synonyms=Menthio;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 ON NCBI_Taxid=10090;
 RN [1]
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).
 RC STPAIN=C57BL/6J; TISSUE=Cerebellum; and Kidney;
 RX MEDLINE=22354683; PubMed=12466851; DOI=10.1038/nature01266;
 RA Okazaki I., Furuno M., Kaikawa T., Adachi J., Bono H., Kondo S.,
 RA Mikaido I., Osato N., Saito R., Suzuki H., Yamanaoka I., Kiyosawa H.,
 RA Yagi K., Tomaru Y., Hasegawa Y., Nogami A., Schenbach C., Gotohori T.,
 RA Baldarelli R., Hill D.P., Bull C., Hume D.A., Quackenbush J.,
 RA Schirral L.M., Kanapin A., Matsuda H., Batalov S., Betzel K.W.,
 RA Blake J.A., Bradt D., Brusic V., Chochia C., Cordan L.E., Cousins S.,
 RA Dalla E., Dragani T.A., Fletcher C.P., Forrest A., Fraser K.S.,
 RA Gaasterland T., Gariboldi M., Gissi C., Godzik A., Gough J.,
 RA Grimwood S., Guetlich S., Hirokawa N., Jackson I.J., Jarvis E.D.,
 RA Kanai A., Kawaji H., Kawasawa Y., Kedzierski R.M., King B.L.,
 RA Konagaya A., Kurochkin I.V., Lee Y., Lenhard B., Lyons P.A.,
 RA Maglott D.R., Maltais L., Marchionni L., McKenzie L., Miki H.,
 RA Nagashima T., Numata K., Okido T., Pavan W.J., Pereira G., Pesole G.,
 RA Petrovsky N., Pillai R., Pontius J.U., Qi D., Ramachandran S.,
 RA Ravasi T., Reed J.C., Reed D.J., Reid J., Ring B.Z., Ringwald M.,
 RA Sandelin A., Schneider C., Sempile C.A., Setou M., Shimada K.,
 RA Sultana R., Takenaka Y., Taylor M.S., Teasdale R.D., Tomita M.,
 RA Verardo R., Wagner L., Wahlstedt C., Wang Y., Watanabe Y., Wells C.,
 RA Wilming L.G., Wyshaw-Boris A., Yamagisawa M., Yang I., Yang L.,
 RA Hyan Z., Zavalan M., Zhu Y., Zimmer A., Carninci P., Hayatsu N.,
 RA Hirozane-Kikihawa T., Kono H., Nakamura M., Sakazume N., Sato K.,
 RA Shiraki T., Waki K., Kawai J., Aizawa K., Arakawa T., Fukuda S.,
 RA Hara A., Hashizume W., Imotani K., Ishii Y., Itoh M., Kagawa I.,
 RA Miyazaki A., Sakai K., Sasaki D., Shibata K., Shinagawa A.,
 RA Yasunishi A., Yoshino M., Waterston R., Lander E.S., Rogers J.,
 RA Birney E., Hayashizaki Y.;
 RT "Analysis of the mouse transcriptome based on functional annotation of
 RT 60,770 full-length cDNAs."
 RL Nature 420:563-573(2002).
 RN [2]
 RP SEQUENCE FROM N.A. (ISOFORM 1).
 RC TISSUE=Brain;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Klausner R.D., Collins F.S., Wagner L., Schaefer C.F., Bhat N.K.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heien F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udell T.B., Toibiyuki S., Carninci P., Pringle C.,
 RA Raha S.S., Loggellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.V., Huijck S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J.J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.B.,
 RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
 CC membrane protein (By similarity).
 CC -1- ALTERNATIVE PRODUCTS:
 CC Event=Alternative splicing; Named isoforms=2;
 CC Name=1;
 CC IsoId=Q9DCI3-1; Sequence=Displayed;
 CC Name=2;

SEQUENCE FROM N.A.

RP TISSUE=Embryo;

RC MEDLINE=22386257; PubMed=12477932; DOI=10.1073/pnas.242603899;

RA Klausberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,

RA Klausberg R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,

RA Diatchenko L., Marnins K., Farmer A.A., Rubin G.M., Hong L.,

RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,

RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carlini P., Prange C.,

RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,

RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,

RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,

RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,

RA Paley U., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,

RA Whiting R.W., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,

RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,

RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,

RA Krzyzanski M.I., Skelske U., Smallus D.E., Scherch A., Schein J.E.,

RA Jones S.J., Mair M.A.,

RA "Generation and initial analysis of more than 15,000 full-length human

RT and mouse cDNA sequences."

RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903 (2002).

RM [2]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Klausberg R.;

RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.

DR EMBL; BC075752; AAH75752.1; --

SO SEQUENCE 227 AA; 25485 MW; 24C46AD8FF4985C6 CRC64;

Query Match 66.6%; Score 796; DB 2; Length 227;

Best Local Similarity 68.3%; Pred. No. 5.1e-64;

Matches 155; Conservative 31; Mismatches 39; Indels 2; Gaps 2;

QY 8 MEMNLTSQSGSHASLRNHSINPTQLMARISYEGREKKGISDVARTFCLPTPTDLPFT 67

DB 1 MDSQSSSVSGSRANDGGAGINSTPISARVESYEGREKKGISDVARTFCLPTPTDLPFT 60

QY 68 LLMTIELLVNNGIENLTLEKEWQDYDYSYDFIPLAVFRFKVLLIYAVCRLRHMAIA 127

DB 61 LLMTIELLVNNGIQOOLEQEVFLKADYHNSFPDIFLPAVFRFAILLIYAVCRLRHMAIA 120

QY 128 LTTAVTSFLLIYAVLSTLFCQAGAGVYLPPIISFLIANIEFWLDFKYLPCQAESENRL 187

DB 121 ITTATTCGFLIVKVVSVKLSQGAFGYLLPIISFLIANIEFWLDFKYLPCQAGDEIRYL 180

QY 188 IVQDASERAAI-IRGLSDQGFVSPPESEAS-EEAEKQSEKPL 232

DB 181 SVQRLEHEPLPPGPISGLFVSPPESLASDSDLDKDLKPIV 227

RESULT 4

Q6DFR7 PRELIMINARY; PRT; 448 AA.

AC Q6DFR7;

DT 25-OCT-2004 (TREMBLrel. 28, Created)

DT 25-OCT-2004 (TREMBLrel. 28, Last sequence update)

DT 25-OCT-2004 (TREMBLrel. 28, Last annotation update)

DE Stard3-prov protein.

GN Name=stard3-prov;

OC Xenopus tropicalis (Western clawed frog) (Silurana tropicalis).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;

OC Xenopodidae; Xenopus.

OX NCBI_TaxID=8364;

OX [1]

RP SEQUENCE FROM N.A.

RC TISSUE=Embryo;

RA Klausberg R.L., Feltingold E.A., Grouse L.H., Derge J.G.,

RA Klausberg R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,

RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitted (JUL-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC076666; AAH76666.1; -
 DR GO; GO:0015485; F:cholesterol binding; IEA.
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
 DR GO; GO:0006694; P:steroid biosynthesis; IEA.
 DR InterPro; IPR000799; SCAR.
 DR InterPro; IPR002913; START.
 DR PRINTS; PRO0978; STARPROTEIN.
 DR SMART; SM00234; START; 1.
 DR PROSITE; PS50848; START; 1.
 SQ SEQUENCE 448 AA; 50926 MW; 2686D07C737D4204 CRC64;
 Query Match 58.6%; Score 700.5; DB 2; Length 448;
 Best Local Similarity 61.1%; Pred. No. 5.2e-55;
 Matches 143; Conservative 29; Mismatches 49; Indels 13; Gaps 4;
 QY 1 MNHLP---EDMENALTGSSSHASLNNHISINPTQLMARIESYEGREKKGISDVRRTPC 56
 1 MTKLPGFQFDLERSLPALASINSMSQNHVFSHSLPR-----BQRVLSVRRTPC 54
 DB 1
 QY 57 LFTVFDLLFTLLMTIELANNNGIENLEKEWQYDYSSYFDIFLAVRFRKVLIIAYA 116
 55 LFTVFDLLFTLLMTIELANNNGIENLEKEWQYDYSSYFDIFLAVRFRKVLIIAYA 114
 DB 117 VCRLRHMAIALTTAVTSAPFLAKVILSKLPSQAGFVLPPIISFIAMETWFLDKPVL 176
 115 IVLRHMAIALTTAVTSAPFLAKVILSKLPSQAGFVLPPIISFIAMETWFLDKPVL 174
 QY 177 PQEAEEENRLLIYQDASERAAI-L-PGGLSDQGFYSPSESEAGEAEKODSEK 229
 175 TQEAEEERWMAVQAGSHPLLVNGLSDQGFYSPSESEAGEAEKODSEK 226
 DB 175

RESULT 5

Q6PFA0 PRELIMINARY; PRT; 444 AA.
 AC O6PFA0;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE MGC68989 protein.
 OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidoidea; Pipidae;
 OC Xenopodidae; Xenopus.
 NCBI_taxid=8355;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=2238825; PubMed=12477937; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold B.A., Grouse L.H., Derge J.G.,
 Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,

RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Ronaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakeley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywinski M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Maira M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RX MEDLINE=22341132; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "Genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT initiative";
 RL Dev. Dyn. 225:384-391(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Spleen;
 RA Klein S., Strausberg R.;
 RL Submitted (SEP-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; BC057738; AAH57738.1; -
 DR GO; GO:0015485; F:cholesterol binding; IEA.
 DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
 DR GO; GO:0006694; P:steroid biosynthesis; IEA.
 DR InterPro; IPR000799; SCAR.
 DR InterPro; IPR002913; START.
 DR PRINTS; PRO0978; STARPROTEIN.
 DR SMART; SM00234; START; 1.
 DR PROSITE; PS50848; START; 1.
 SQ SEQUENCE 444 AA; 50572 MW; 7BEA97317BF48358 CRC64;
 Query Match 58.5%; Score 698.5; DB 2; Length 444;
 Best Local Similarity 60.9%; Pred. No. 7.9e-55;
 Matches 140; Conservative 30; Mismatches 51; Indels 9; Gaps 3;
 QY 1 MNHLPEDMENALTGSSSHASLNNHISINPTQLMARIESYEGREKKGISDVRRTPC 60
 1 MTKLPGFQFDLERSLPALASMSQSHVFSRSLPR-----BQRALISVRRTPC 54
 DB 1
 QY 61 FDLFTVLLMTIELANNNGIENLEKEWQYDYSSYFDIFLAVRFRKVLIIAYVCR 120
 55 FDLFTVLLMTIELANNNGIENLEKEWQYDYSSYFDIFLAVRFRKVLIIAYVCR 114
 DB 121 RHWMAIALTTAVTSAPFLAKVILSKLPSQAGFVLPPIISFIAMETWFLDKPVL 180
 115 RHWMAIALTTAVTSAPFLAKVILSKLPSQAGFVLPPIISFIAMETWFLDKPVL 174
 QY 181 EENRRLLIYQDASERAAI-L-PGGLSDQGFYSPSESEAGEAEKODSEK 229
 175 EEBRWYIAQAAATPHSLLVNGLSDQGFYSPSESEAGEAEKODSEK 222
 DB 175

RESULT 6

Q6GNT3 PRELIMINARY; PRT; 448 AA.
 ID Q6GNT3;
 DT 05-JUL-2004 (Tremblrel. 27, Created)
 DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
 DE MGC80895 protein.
 GN Name=MGC80895;

OS Xenopus laevis (African clawed frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipidae; Pipidae;
 OC Xenopodinae; Xenopus.
 NCBI TaxID=8355;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.; analysis of more than 15,000 full-length human
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RX MEDLINE=2231113; PubMed=12454917; DOI=10.1002/dvdy.10174;
 RA Klein S.L., Strausberg R.L., Wagner L., Pontius J., Clifton S.W.,
 RA Richardson P.;
 RT "genetic and genomic tools for Xenopus research: The NIH Xenopus
 RT Initiative."
 RL Dev. Dyn. 225:384-391(2002).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Embryo;
 RA Klein S., Gerhard D.S.;
 RL Submitt (JUN-2004) to the EMBL/GenBank/DBJ databases.
 RX EMBL: BC073419; AAT73419.1; -
 DR GO: GO:0015485; F:cholesterol binding; IEA.
 DR GO: GO:0017127; F:cholesterol transporter activity; IEA.
 DR GO: GO:0006694; P:steroid biosynthesis; IEA.
 DR InterPro: IPR000799; STAR.
 DR InterPro: IPR002913; STAR.
 DR Pfam: PF01852; START; 1.
 DR PRINTS: PR00978; STARPROTEIN.
 DR SMART: SM00234; START; 1.
 DR PROSITE: PS50848; START; 1.
 DR PROSITE: PS50848; START; 1.
 SQ SEQUENCE 448 AA; 51279 MW; 472PF8E7C3B2584 CRC64;
 Query Match 57.2%; Score 684; DB 2; Length 448;
 Best Local Similarity 59.7%; Pred. No. 1.6e-53;
 Matches 139; Conservative 34; Mismatches 48; Indels 12; Gaps 4;
 QY 1 MNHLP-----EDMENALTSQSASHALRNHNSINPTQLMARIESYEGKKGISDVRTPFC 56
 DB 1 MTLPLGFQFDLRLSLPALASINSNGHNVFPHSLPR-----QRLLISIVRTTFC 54
 QY 57 LPTVFDLLPTLLMTIELNNGIGIENTLEKVMQDYDYSSFDIPELLAVFRPKYLLIAYA 116
 DB 55 LPTVFDLLPTLLMTIELNNGIGIENTLEKVMQDYDYSSFDIPELLAVFRPKYLLIAYA 114
 QY 117 VCGRLHMMALATTAATVSAFLAKVILSKLFSQAGFVPLPIISFLIAMIETWPLDKVL 176
 DB 115 IVRRHMMALATTAATVSAFLAKVILSKLFSQAGFVPLPIISFLIAMIETWPLDKVL 174
 QY 177 POAEENRLLIVQ-DASERRAALIPGGLSDGQFSPESPESGSE-BAEEKSDS 227

DB 175 POAEENRWTAAQADANHPPLYNGLTSDGQFSPESPESGSDNEFEDEEA 227
 RESULT 7
 ID ML64 HUMAN STANDARD; PRT; 445 AA.
 AC 014849; 096HM9;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 23-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE MLN 64 protein (STAR-related lipid transfer protein 3) (START3) (START
 GN Name=START3; Synonyms=CAB1, MLN64;
 OS Homo sapiens (human).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 NCBI TaxID=9606;
 [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast carcinoma;
 RX MEDLINE=96039245; PubMed=7490069;
 RA Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
 RA Chénard M.-P., Lideanu R., Bassot P., Rio M.-C.;
 RT "Identification of four novel human genes amplified and overexpressed
 RT in breast carcinoma and localized to the q11-q21.3 region of
 RT chromosome 17."
 RL Genomics 28:367-376(1995).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Oesophageal carcinoma;
 RX MEDLINE=97413641; PubMed=9270027;
 RA Akiyama N., Sasaki H., Ishizuka T., Kishi T., Sakamoto H., Onda M.,
 RA Hirai H., Yazaki Y., Sugimura T., Terada M.;
 RT "Isolation of a candidate gene, CAB1, for cholesterol transport to
 RT mitochondria from the c-SRB-2 amplicon by a modified cDNA selection
 RT method."
 RL Cancer Res. 57:3548-3553(1997).
 [3]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Lung, Skin, and Spleen;
 RX MEDLINE=2238825; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusik K., Farmer A.A., Rubin G.M., Hong L.,
 RA Brownstein M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tothiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettman M., Madan A., Rodriguez S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywiński M.I., Skalska U., Smalins D.E., Schnerch A., Schein J.E.,
 RA Jones S.J., Marra M.A.; analysis of more than 15,000 full-length human
 RT "generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences."
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 [4]
 RP X-RAY CRYSTALLOGRAPHY (2.2 ANGSTROMS) OF 216-445
 RX MEDLINE=20264523; PubMed=10802740; DOI=10.1038/75192;
 RA Teufelschlä Y., Hurley J.H.;
 RT "Structure and lipid transport mechanism of a STAR-related domain."
 RL Nat. Struct. Biol. 7:408-414(2000).
 [5]
 RP TOPOLOGY
 RX MEDLINE=11053434; DOI=10.1074/jbc.M006279200;
 RA Alpy F., Stoeckel M.-E., Dietrich A., Escola J.-M., Wendling C.,
 RA Chénard M.-P., Vanier M.T., Gruenberg J., Tomasetto C., Rio M.-C.;
 RT "The sterologenic acute regulatory protein homolog MLN64, a late

RT endosomal cholesterol-binding protein.";
 RL J. Biol. Chem. 276:4261-4269(2001).
 CC -1- FUNCTION: Binds and transports cholesterol. Promotes
 steriodogenesis in placenta and brain.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
 membrane protein.
 CC -1- SIMILARITY: Contains 1 MENTAL domain.
 CC -1- SIMILARITY: Contains 1 START domain.
 CC -1- DATABASE: NAMB-Atlas Genet. Cytoget. Haematol.;
 WWW="http://www.infobio.gen.fr/services/chromosome/gene/MN641D202.html".
 CC -----
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 or send an email to license@ebi.ac.uk).
 CC -----
 DR EMBL: X80198; CA56489.1; -;
 DR EMBL: D38255; BAA22525.1; -;
 DR EMBL: BC008356; AAH08356.1; -;
 DR EMBL: BC008747; AAH08747.1; -;
 DR EMBL: BC025679; AAH25679.1; -;
 DR PIR: I38027; I38027.
 DR PDB: 1EM2; X-ray; A=216-444.
 DR Genew: HGNC:17579; STARD3.
 DR H-InvDB: HIK0013780; -;
 DR MTM: 607048; -;
 DR GO: GO:0005737; C:cytoplasm; TAS.
 DR GO: GO:0008203; P:cholesterol metabolism; TAS.
 DR GO: GO:0006839; P:mitochondrial transport; TAS.
 DR GO: GO:0008202; P:steroid metabolism; TAS.
 DR InterPro: IPR007999; SCAR.
 DR InterPro: IPR002913; START.
 DR Pfam: PF01852; START; 1.
 DR PRINTS: PR00978; STARPROTEIN.
 DR SMART: SM00234; START; 1.
 DR PROSITE: PS50848; START; 1.
 KW 3D-structure; Lipid transport; Lipid-binding; Steroidogenesis;
 KM Transmembrane; Transport.
 FT DOMAIN 1 51
 FT TRANSSEM 52 72 Cytoplasmic (Potential).
 FT TRANSSEM 73 94 Potential.
 FT TRANSSEM 95 115 Extracellular (Potential).
 FT TRANSSEM 116 120 Potential.
 FT TRANSSEM 121 141 Cytoplasmic (Potential).
 FT TRANSSEM 142 148 Potential.
 FT TRANSSEM 149 169 Extracellular (Potential).
 FT DOMAIN 170 445 Potential.
 FT DOMAIN 46 217 Cytoplasmic (Potential).
 FT DOMAIN 230 443 START.
 FT CONFLICT 117 117 Q -> R (in Ref. 3; AAH08356/AAH25679).
 FT CONFLICT 216 216 G -> A (in Ref. 3; AAH25679).
 FT HELIX 233 253
 FT TURN 254 255
 FT HELIX 256 258
 FT STRAND 260 264
 FT TURN 266 267
 FT STRAND 270 276
 FT TURN 277 279
 FT STRAND 280 289
 FT STRAND 293 299
 FT HELIX 300 302
 FT TURN 304 307
 FT HELIX 308 310
 FT TURN 312 313
 FT STRAND 314 323
 FT TURN 324 326
 FT STRAND 327 334
 FT STRAND 337 337
 FT TURN 338 341
 FT STRAND 342 342

FT STRAND 345 355
 FT STRAND 359 366
 FT TURN 370 371
 FT TURN 376 377
 FT STRAND 379 380
 FT STRAND 382 383
 FT STRAND 386 392
 FT TURN 397 398
 FT STRAND 400 406
 FT STRAND 408 409
 FT HELIX 416 440
 FT TURN 441 442
 SQ SEQUENCE 445 AA; 50474 MW; 62BED5C3EAD0DEF CRC64;
 Query Match 55.6%; Score 664; DB 1; Length 445;
 Best Local Similarity 56.2%; Pred. No. 1.1e-51;
 Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;
 QY 1 MNHLP---EDMENAL-----TGSQSHASLRNHSINPTQLMARIESYBGRKKGISDV 51
 DB 1 MSKLPRLTRDLRSLPAVASLSSLSHSQSLSHLPPE-----KRAISDV 49
 QY 52 RRTFCLFVTFDLFISLWITELNVTGIRKNLEQETIQNFKTSFFDLVLPFRSGL 111
 DB 50 RRTFCLFVTFDLFISLWITELNVTGIRKNLEQETIQNFKTSFFDLVLPFRSGL 109
 QY 112 ILAVAVCRLRHMAIALTTVAFTSAFLAKVLSKLPSCGAFGVLPISPIAMIETWL 171
 DB 110 LIGAVVLQLRHMAIALTTVAFTSAFLAKVLSKLPSCGAFGVLPISPIAMIETWL 169
 QY 172 DFFVLPQEAERERKLLIVDASERALL-PCGISDQGFYPPPSSEAGSE-FAEEKQDSEK 229
 DB 170 DFFVLPQEAERERKLLIVDASERALL-PCGISDQGFYPPPSSEAGSE-FAEEKQDSEK 229
 RESULT 8
 ML64_MOUSE STANDARD; PRT; 446 AA.
 AC 061542;
 DT 30-MAY-2000 (Rel. 39, Created)
 DT 30-MAY-2000 (Rel. 39, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE MLN 64 protein (StAR-related lipid transfer protein 3) (STARD3) (START
 domain-containing protein 3) (BS 64 protein).
 GN Name=Stard3; Synonyms=Bs64, MLN64;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=6039245; PubMed=7490069;
 RA Tomasetto C.L., Regnier C.H., Moog-Lutz C., Mattei M.-G.,
 RA Chenard M.-P., Lidereau R., Basset P., Rio M.-C.,
 RT "Identification of four novel human genes amplified and overexpressed
 in breast carcinoma and localized to the q11-q21.3 region of
 chromosome 17.";
 RL Genomics 28:367-376 (1995).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Breast;
 RX MEDLINE=23388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strauberg R.L., Peingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Schetz T.E.,
 RA Brownstein M.J., Uedin T.B., Tohbiyuki S., Carninci P., Prange C.,
 RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Muliyil S.J.,
 RA Bosak S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulik S.W.,
 RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu K., Gibbs R.A.,

RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Butterfield Y.S.N., Krzywnicki M.I., Skalek U., Smalins D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Maria M.A.,
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: Binds and transports cholesterol. Promotes
 CC steroidogenesis in placenta and brain (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Late endosomal
 CC membrane protein (By similarity).
 CC -1- SIMILARITY: Contains 1 MEMBRAN domain.
 CC -1- SIMILARITY: Contains 1 START domain.
 CC -----
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 CC -----
 CC EMBL: X82457; CA57834.1; -.
 CC EMBL: BC003313; AAH03313.1; -.
 CC HSSP: Q14848; 1EM2.
 CC MGD: MGI:1929618; Stard3.
 CC InterPro: IPR000799; STAR.
 CC InterPro: IPR002913; STAR.
 CC Pfam: PF01852; START; 1.
 CC PRINTS: PR00978; STARRPROTEIN.
 CC SMART: SM00234; START; 1.
 CC PROSITE: PS00848; START; 1.
 CC KX Lipid transport; lipid-binding; Steroidogenesis; Transmembrane;
 CC Transport.
 CC KM DOMAIN 1 52 Cytoplasmic (Potential).
 CC FT TRANSMEM 53 73 Potential.
 CC FT TRANSMEM 74 95 Extracellular (Potential).
 CC FT TRANSMEM 96 116 Potential.
 CC FT TRANSMEM 117 121 Cytoplasmic (Potential).
 CC FT TRANSMEM 122 142 Potential.
 CC FT TRANSMEM 143 149 Extracellular (Potential).
 CC FT TRANSMEM 150 170 Potential.
 CC FT DOMAIN 171 446 Cytoplasmic (Potential).
 CC FT DOMAIN 47 218 Potential.
 CC FT DOMAIN 231 444 START.
 CC SQ SEQUENCE 446 AA; 50469 MW; DBF4359604F3E1E2 CRC64;
 Query Match 54.9%; Score 656.5; DB 1; Length 446;
 Best Local Similarity 57.8%; Pred. No. 5.1e-51;
 Matches 133; Conservative 33; Mismatches 47; Indels 17; Gaps 4;
 QY 7 DMENAL-----TSSQSSHASLRNHSINPTQLMARIESYEGREKGGIDVRRTECLFVT 61
 Db 11 DLERSLPALASLSTSHSGLSHSRTPPL-----EKRAISDVRRTECLFVT 60
 QY 62 DLLFVTLMTIELNVNGGIENTLEKEVMQDYSSYDFLLAVFRFKVLIILAVACRLR 121
 Db 61 DLLFISLMTIELNTNGIRKNEIQEVIHYSFQSPFDIFVLAFPRSGILLGAVARLQ 120
 QY 122 HMAAALTTAVTSAPFLAKVILSKLPSQAGVYLPIISFTLMIEMWFLDFKVLPOEAR 161
 Db 121 HMAVIAATTVSSAPFLVAVILSKLPSQAGVYLPIISFTLMIEMWFLDFKVLPOEAR 160
 QY 182 EENRLILVODASERAAI-EGSLSDGQFYSPPSSEAGSE-EAEKQDSEK 229
 Db 181 EENWYLAQAQAVARGPLLPSGALSGEQFYSPPSSEAGSDNDSDEVTGKK 230

AC Q6PH03;
 DT 05-JUL-2004 (TrEMBLrel. 27, Created)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
 DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
 DE START domain containing 3.
 GN Name=stard3;
 OS Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.
 OC NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
 RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buettow K.H., Schaefer C.F., Bhat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Heile F.,
 RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Ueda T.B., Toshiyuki S., Carninci P., Prange C.J.,
 RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullany S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hultk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
 RA Krzywnicki M.I., Skalek U., Smalins D.E., Scherch A., Schein J.E.,
 RA Jones S.J., Maria M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human
 RT and mouse cDNA sequences";
 RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=AB; TISSUE=whole body;
 RA Strausberg R.,
 RL Submitted (Aug-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL: BC056766; AAH56766.1; -.
 DR ZFIN: ZDB-GENE-001120-2; stard3.
 DR GO: GO:0015485; F:cholesterol binding; IEA.
 DR GO: GO:0017127; F:cholesterol transporter activity; IEA.
 DR GO: GO:0006694; P:steroid biosynthesis; IEA.
 DR InterPro: IPR000799; STAR.
 DR InterPro: IPR002913; STAR.
 DR Pfam: PF01852; START; 1.
 DR PRINTS: PR00978; STARRPROTEIN.
 DR SMART: SM00234; START; 1.
 DR PROSITE: PS00848; START; 1.
 DR SQ SEQUENCE 448 AA; 50751 MW; 716A18C127B59C5D CRC64;
 Query Match 52.9%; Score 632; DB 2; Length 448;
 Best Local Similarity 70.9%; Pred. No. 8.6e-49;
 Matches 127; Conservative 18; Mismatches 32; Indels 2; Gaps 2;
 QY 44 EKKGISDVRRTFCLFVTFDILLFTLLMIETLVNNGGIENTLEKEVMQDYSSYDFLL 103
 Db 43 ERRAFDVRRTECLFVTFDILLFTLLMIETLVNNGGIENTLEKEVMQDYSSYDFLL 102
 QY 104 AVRFKVLIAAVVCGLRHMMVAITLTAVTASFLAKVILSKLPSQAGVYLPIISFIL 163
 Db 103 AVRFKVLIAAVVCGLRHMMVAITLTAVTASFLAKVILSKLPSQAGVYLPIISFIL 162
 QY 164 AMIETWFLDFKVLPOEAR-RLILVODASERAAI-EGSLSDGQFYSPPSSEAGSE 220
 Db 163 AMIETWFLDFKVLPOEAR-RLILVODASERAAI-EGSLSDGQFYSPPSSEAGSE 221

RESULT 9
 Q6PH03
 ID Q6PH03 PRELIMINARY; PRT; 448 AA.

RESULT 10
 Q8BMP8
 ID Q8BMP8 PRELIMINARY; PRT; 107 AA.

AC Q8BMP8;
DT 01-MAR-2003 (TrEMBLrel. 23, Created)
DT 01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
DE Mus musculus adult male pituitary gland cDNA, RIKEN full-length
DE enriched library, clone:530402M06 product:H.NH021A08.1 PROTEIN
DE (UNKNOWN) (PROTEIN FOR MGC:14607) (SIMILAR TO STEROIDGENIC ACUTE
DE REGULATORY PROTEIN RELATED) homolog.
OS Mus musculus (Mouse).
OC Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=99279253; PubMed=10349636; DOI=10.1016/S0076-6879(99)03004-9;
RA Carmichael P., Hayashizaki Y.;
RT "High-efficiency full-length cDNA cloning.";
RL Mech. Enzymol. 303:19-44(1999).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=21085660; PubMed=11217851; DOI=10.1038/35055500;
RA RIKEN FANTOM Consortium;
RT "Functional annotation of a full-length mouse cDNA collection.";
RL Nature 409:685-690(2001).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RA The FANTOM Consortium;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT 60,770 full-length cDNAs.";
RL Nature 420:563-573(2002).
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=20499374; PubMed=11042159; DOI=10.1101/gr.145100;
RA Carmichael P., Shihata Y., Hayatsu N., Sugahara Y., Shihata K., Itoh M.,
RA Kono H., Okazaki Y., Muramatsu M., Hayashizaki Y.;
RT "Normalization and subtraction of cap-trapper-selected cDNAs to
RT prepare full-length cDNA libraries for rapid discovery of new genes.";
RL Genome Res. 10:1617-1630(2000).
RN [5]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RC MEDLINE=20530913; PubMed=11076861; DOI=10.1101/gr.152600;
RA Shihata K., Itoh M., Aizawa K., Nagasaka S., Sasaki N., Carmichael P.,
RA Kono H., Akiyama J., Nishi K., Kitasuna T., Tashiro H., Itoh M.,
RA Sumi N., Ishii Y., Nakamura S., Hazama M., Nishine T., Harada A.,
RA Yamamoto R., Matsunoto H., Sakaguchi S., Ikegami T., Kashiwagi K.,
RA Fujisawa S., Inoue K., Togawa Y., Izawa M., Ohara E., Matsuki M.,
RA Yoneda Y., Ishiura T., Ozawa K., Tanaka T., Matsura S., Kawai J.,
RA Okazaki Y., Muramatsu M., Inoue Y., Kira A., Hayashizaki Y.;
RT "RIKEN integrated sequence analysis (RISA) system-384-format
RT sequencing pipeline with 384 multicapillary sequencer.";
RL Genome Res. 10:1757-1771(2000).
RN [6]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6J; TISSUE=pituitary gland;
RA Adachi J., Aizawa K., Akimura T., Arikawa T., Bono H., Carmichael P.,
RA Fukuda S., Furuno M., Hanagaki T., Hara A., Hashizume W.,
RA Hayashida K., Hayatsu N., Hiramoto K., Hirooka T., Hirozane T.,
RA Horii F., Imocant K., Ishii Y., Itoh M., Kagawa I., Kasukawa T.,
RA Kato H., Kawai J., Kojima Y., Kondo S., Kono H., Kouda M., Koya S.,
RA Kurihara C., Matsuyama T., Miyazaki A., Murata M., Nakamura M.,
RA Nishi K., Nomura K., Numazaki R., Ono M., Ohnaka N., Okazaki Y.,
RA Saito R., Satoh H., Sakai C., Sakai K., Sakazume N., Sano H.,
RA Sasaki D., Shihata K., Shinagawa A., Shiraki T., Sogabe Y., Tagami M.,
RA Takagawa A., Takahashi F., Takaku-Akahira S., Takeda Y., Tanaka T.,
RA Tomaru A., Toyota T., Yasunishi A., Muramatsu M., Hayashizaki Y.;
RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR EMBL; AK030365; BAC26922.1; -.

SQ SEQUENCE 107 AA; 12417 MW; 1B30DA6C81469089 CRC64;
Query Match 41.2%; Score 492; DB 2; Length 107;
Best Local Similarity 92.2%; Pred. No. 8.2e-37;
Matches 94; Conservative 4; Mismatches 4; Indels 0; Gaps 0;
QY 1 MNHLPEDMENALTGSSGSHASLNHISINPTQLMARIESYEGREKGISVRRTPCLFVT 60
DB 1 MNHLPEDMENALTGSSGSHASLNHISINPTQLMARIESYEGREKGISVRRTPCLFVT 60
QY 61 FDLFPVTLMTIELNVNGIENTLEKEVMQDYSSYFDLFL 102
DB 61 FDLFPVTLMTIELNVNGIENTLEKEVMQDYSSYFDLFL 102

RESULT 11

Q7QIT3 PRELIMINARY; PRT; 568 AA.
AC Q7QIT3;
DT 01-MAR-2004 (TrEMBLrel. 26, Created)
DT 01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
DE AGCP3158 (Fragment).
GN Name=agc32468; ORFNames=ENSG000000018959;
OS Anopheles gambiae Str. FST.
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Nematocera; Culicoidae; Anopheles.
OX NCBI_TaxID=180454;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=PEST;
RA Anopheles Genome Sequencing Consortium;
RL Submitted (MAR-2002) to the EMBL/GenBank/DBJ databases.
CC -1- CAUTION: The sequence shown here is derived from an
CC EMBL/GenBank/DBJ whole genome shotgun (WGS) entry which is
CC preliminary data.
DR EMBL; AAB0100807; EAA03945.1; -
DR GO; GO:0015485; F:cholesterol binding; IEA.
DR GO; GO:0017127; F:cholesterol transporter activity; IEA.
DR GO; GO:0006694; P:steroid biosynthesis; IEA.
DR InterPro: IPR000799; SCAR.
DR InterPro: IPR002913; START.
DR PRINTS; PR00976; STARRPROTEIN.
DR PROSITE; PSS0848; START; 1.
FT NON TER 1
FT NON TER 568
SQ SEQUENCE 568 AA; 62932 MW; ECB3D361A05DF15 CRC64;

Query Match 29.1%; Score 348; DB 2; Length 568;
Best Local Similarity 36.6%; Pred. No. 6.7e-23;
Matches 86; Conservative 45; Mismatches 72; Indels 32; Gaps 9;

QY 13 TGSOSHASLRNHSINPTQLMAR--IESYEGREKGISVRRTPCLFVTDLFLVTLW 70
DB 1 TRQS-----HYN--LISEDTAG--MEGRMSVRRPCLFVTDFVFLSLW 47
QY 71 IIELVNNG-GIENTLEKEVMQDYSSYFDLFLAVFRFVLLAAYAVCLRHMALAT 129
DB 48 IICVITGDVNHVHALQOVHLYVYTSLFDVIAALIRFLILFGLISISHMLVIALS 107
QY 130 TAVTSAPLAKVLKSLFS--QCAFQVLPPIISFILAMFTWLDKRVLPQEAEEENRL 167
DB 108 TTSCAFILSKVPLVDMTAPQVFFVLIVSFVLAMGAWPLDCKVLPQERYARYFV 167
QY 188 IYVDASBRALIP-----GGLSD--GQFYSPES--RAGSEBAEKQDSE 228
DB 168 AITNPGSMARPTLPLPFLSAMQAGRTESIGNYSPDSIHNSDDDDDDDDDDQDDE 222

RESULT 12

Q8MZ4 PRELIMINARY; PRT; 545 AA.
AC Q8MZ4;
Q8MZ4;

DT 01-OCT-2002 (TrEMBLrel. 22, Created)
 DT 01-OCT-2002 (TrEMBLrel. 22, Last sequence update)
 DT 25-OCT-2004 (TrEMBLrel. 28, Last annotation update)
 DE LD23690P (CG3522-PB).
 GN ORFNames=CG3522;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 NCBI_TaxID=7227;
 RN
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayan A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Fatfan D., Frise E.,
 RA George R., Gonzales M., Gaurin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Nunoo J., Pacleb J., Paragas V., Park S.,
 RA Patel S., Phouanavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celniker S.;
 RA Submitted (MAY-2002) to the EMBL/GenBank/DBJ databases.
 [2]
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20196006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoekstra R.A., Galie R.F.,
 RA George R., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Baller R.M., Baau A.V., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burdys J.C., Busam D.A., Butler H., Caden E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke S., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Dou P.L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferlita S., Fleischmann W.,
 RA Froder C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodde A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Houtin D., Houston K.A., Howland T.J., Wei M.H., Ibeagwa C.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Laoko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Matei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Stryer E., Stradling A.C., Stapleton M., Strong R., Sun B.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weisenbach G.M., Weisenbach J.,
 RA Williams S.M., Woodrager W., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yen R.F., Zaveri U.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zeng X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers B.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of Drosophila melanogaster";
 RL Science 287:2185-2195(2000).
 RN
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A.,
 RA George R.A., Hoekstra R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Pacleb J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weisenbach G., Scherter S.E., Myers B.W., Gibbs R.A., Rubin G.M.,
 RT "Finishing a whole-genome shotgun: Release 3 of the Drosophila
 melanogaster euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).

RN
 RP [4]
 RX MEDLINE=22426070; PubMed=12537573;
 RA Kaminiker J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the Drosophila melanogaster euchromatin:
 a genomics perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN
 RP [5]
 RX MEDLINE=22426069; PubMed=12537572;
 RA Miera S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminiker J.S., Millburn G.H., Prochuk S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bergman B.B.,
 RA Battencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Ruseo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the Drosophila melanogaster euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN
 RP [6]
 RX SEQUENCE FROM N.A.
 RG FlyBase;
 RN Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 [7]
 RN
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RX Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AY024683; AAM27512.1; -;
 DR EMBL: AB003464; AAM64770.1; -;
 DR FlyBase; FBgn0035028; CG3522.
 DR GO: GO:0015485; F:cholesterol binding; IEA.
 DR GO: GO:0017127; F:cholesterol transporter activity; IEA.
 DR GO: GO:0006994; P:steroid biosynthesis; IEA.
 DR InterPro: IPR000799; STAR.
 DR InterPro: IPR002913; STAR.
 DR PRINTS: PRO0978; STARPROTEIN.
 DR PROSITE: PS50848; START; 1.
 DR SEQUENCE 545 AA; 61429 MW; 5F6EA99AC917160 CRC64;
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 Query Match 28.7%; Score 343; DB 2; Length 545;
 Best Local Similarity 37.8%; Pred. No. 1.8e-22;
 Matches 90; Conservative 44; Mismatches 76; Indels 28; Gaps 10;
 QY 8 MENALTGSSGSHA--SLRNHISINPTQLMARISYEGREKKG--ISDVRRTFCLEFVFDLL 64
 DB 17 LANARQNSAYNNQYDMSRAHSIN-----LITDFLAGVWQDGMSTVRRFFCLFVFDLV 72
 QY 65 FVTLNLTIELNANG-GIENTLEKXWQYDYSSYDFILAVRFKYLILAYAVCRLRW 123
 DB 73 FVSLNLTICIVINDGIFFAFHKOIVEYTYKLPFDVAVALRFLVLIFFVAILYINHW 132
 QY 124 WATALTAVAVSAFLAKVIL-----SKLFGQAGFVYLPIISFLAMIEFTWPIDFKVL 178
 DB 133 STIALSTSGCLFLISKVFVFWLDSK--QQVFVILITTSITLILNGEMFLDCRYIPQ 189
 QY 179 E--AEENRLLIVQDAS--ERALLI-----PGSLSDGQFSPPESEAGSEAEKOD 226
 DB 190 ERHAGHFRTMTSNDRTPEMQPALILEQERFPQSVTD--FYSIMDTVRHSDEDELD 245
 RESULT 13
 ID Q9W145 PRELIMINARY; PRT; 583 AA.
 AC Q9W145;
 DT 01-MAY-2000 (TrEMBLrel. 13, Created)
 DT 25-OCT-2004 (TrEMBLrel. 13, Last sequence update)
 DE CG3522-PA (Putative cholesterol transporter).
 GN ORFNames=CG3522;
 OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7227;
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 RX MEDLINE=20156006; PubMed=10731132; DOI=10.1126/science.287.5461.2185;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.B., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazer V., Champs M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA April J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.V., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotter P.,
 RA Burlis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrier S., Fleischmann W.,
 RA Fessler C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glöckner A., Gong F., Gottrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jallat M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusekern D.R., Paclob J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Weissman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodger, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang X., Zhao Q., Zheng L.,
 RA Zheng X.H., Zheng F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 RN [2]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426065; PubMed=12537568;
 RA Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halpern A.,
 RA Patel S., Adams M., Champe M., Dugan S.P., Frishe B., Hodgson A.,
 RA George R.A., Hoskins R.A., Laverly T., Muzny D.M., Nelson C.R.,
 RA Paclob J.M., Park S., Pfeiffer B.D., Richards S., Sodergren E.J.,
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C.,
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.;
 RT "Finishing a whole-genome shotgun: Release 3 of the *Drosophila*
 RT *melanogaster* euchromatic genome sequence.";
 RL Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
 RN [3]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426070; PubMed=12537573;
 RA Krimm J.S., Bergman C.M., Krommiller B., Carlson J., Svirskas R.,
 RA Patel S., Frishe B., Wheeler D.A., Lewis S.E., Rubin G.M.,
 RA Ashburner M., Celniker S.E.;
 RT "The transposable elements of the *Drosophila melanogaster* euchromatin:
 RT a genomic perspective.";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084(2002).
 RN [4]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Kaminker J.S., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield B.J., Bayraktaroglu L., Berman B.P.,
 RA Betencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 RT systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083(2002).
 RN [5]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RX FLYBASE;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RX PubMed=14745013; DOI=10.1073/pnas.0308212100;
 RA Roth G.E., Gierl M.S., Vollborn L., Meise M., Lintemann R., Korge G.,
 RT "The *Drosophila* gene *Starl* is a putative cholesterol transporter and
 RT key regulator of ecdysteroid synthesis.";
 RL Proc. Natl. Acad. Sci. U.S.A. 101:1601-1606(2004).
 DR EMBL: AE003464; AAF47232.2; -;
 DR EMBL: AY455866; AAR19767.1; -;
 DR InAct: Q9W145; -;
 DR FLYBASE: FBgn0035028; CG3522.
 DR GO: GO:0015485; F:cholesterol binding; IEA.
 DR GO: GO:0017127; F:cholesterol transporter activity; IEA.
 DR GO: GO:0006694; P:steroid biosynthesis; IEA.
 DR InterPro: IPR000799; STAR.
 DR InterPro: IPR002913; START.
 DR Pfam: PF01852; START.
 DR PRINTS: PR00978; STARPROTEIN.
 DR PROSITE: PSS0848; START.
 SQ SEQUENCE 583 AA; 65822 MW; F043047A5AD6DFP1 CRC64;
 Query Match 28.7%; Score 343; DB 2; Length 583;
 Best Local Similarity 37.8%; Pred. No. 26-22;
 Matches 90; Conservative 44; Mismatches 76; Indels 28; Gaps 10;
 QY 8 MENALNGSOSHA--SLRNHSINPTOLMARISYGRKKG-ISPDRPTFCFTFDLL 64
 DB 17 LANARQNSAYNQYDMSRAHSIN---LITEFLAGYQDGMSTVRRFCFTFDLV 72
 QY 65 FVTLLMIIELVNG-GIENTLEKXVQYDYSYFDIFLAVRRFVLLIAYVCRRLRW 123
 DB 73 FVSLMLVICIVNGDINFTAFHKQIVETIKSLFDVAVACRFLVIFPVALYNHW 132
 QY 124 WALALTAVTSATLAKVL-----SKLPQGFVGLVPIISITLMIETWPIDFVL 178
 DB 133 SIATLSGSCPLRLSKVFFVFWLDSK--QVFEVILLITSPILMGEAMFLDCRVLPQ 189
 QY 179 E--AEENRLLIYQDAS--ERALLI-----PGLSDGQFSPSEBAGSEAEKRD 226
 DB 190 ERRAQHYFRMTSNDRTPEQPAILLRQERFPQSVTD--FYSIMDTARRHSDDEDD 245
 RESULT 14
 ID 019819 PRELIMINARY; PRT; 447 AA.
 AC 019819;
 DT 01-NOV-1996 (TEMBLrel. 01, Created)
 DT 01-OCT-2002 (TEMBLrel. 22, last sequence update)
 DT 01-MAR-2004 (TEMBLrel. 26, last annotation update)
 DE Hypothetical protein F26F4.4.
 OS ORFNames=F26F4.4, F26F4.4;
 GN Caenorhabditis elegans.
 OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditioidea;
 OC Rhabditidae; Pelodierinae; Caenorhabditis.
 OC NCBI_TaxID=6239;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX STRAIN=Brictol N2;
 MEDLINE=99069613; PubMed=9851916;

RG Wormbase Consortium;
 RT "Genome sequence of the nematode C. elegans: a platform for
 RT investigating biology. The C. elegans Sequencing Consortium.";
 RL Science 282:2012-2018(1998).
 RL [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Br1sc01 N2;
 RA Pullon L.;
 RT "The sequence of C. elegans cosmid F26F4.";
 RL Submitted (NOV-1994) to the EMBL/GenBank/DBJ databases.
 RL [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Br1sc01 N2;
 RA Waterston R.;
 RL Submitted (NOV-2002) to the EMBL/GenBank/DBJ databases.
 RL [4]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Br1sc01 N2;
 RA Wilson R.;
 RL Submitted (NOV-2003) to the EMBL/GenBank/DBJ databases.
 RL [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Br1sc01 N2;
 RG Wormbase Consortium;
 RL Submitted (AUG-2004) to the EMBL/GenBank/DBJ databases.
 DR EMBL; U12964; AAA91219.3; -.
 DR PIR; T16170; T16170.
 DR Wormbase; WBGene00017826; F26F4.4.
 DR WormPep; F26F4.4; CE30767.
 DR InterPro; IPR002913; START.
 DR Pfam; PF01852; START; 1.
 DR SMART; SM00234; START; 1.
 DR PROSITE; PSS0848; START; 1.
 DR Hypothetical protein.
 KW SEQUENCE 447 AA; 51543 MW; D863948844670113 CRC64;
 SQ
 Query Match 17.1%; Score 204; DB 2; Length 447;
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 Matches 56; Conservative 36; Mismatches 73; Indels 46; Gaps 6;
 QY 42 GREKGISDVRTPCLFVTPDLLFVTLMTI-----ELNVNGIETLEK 86
 DB 11 GSQRIGVSKDKRPFIVTFDTISITLLMLCTVTRDDWDKVFNEINI-----FNP 63
 QY 87 EVMQYDYSSYPDIFLAAYRFRKVLILAYACRLRHMAIALTTAAVTSAPLLAKVILSKL 146
 DB 64 KFLRI-----SLFDIVLLAVLRMLILGVYGLVQKQWYVAFTTLASSAYILMKVLFYFN 119
 QY 147 PSQAGFGYVPLI-SFILAMIEFTWFLDFKVLPOEAEENRLLIVQASERAAIIPGLSD 205
 DB 120 HSSSAVPEPLLIITTSFTLCSEFTLMPFQILPRERARREL-----DGIEN 166
 QY 206 GQFYSPPESEA-----GSEAEAEKQDEKP 230
 DB 167 PEPSTDDARSNNRRRGRQNGSQSEAP 197
 RESULT 15
 ML64_SALFO STANDARD; PRT; 294 AA.
 AC 0902B9;
 DT 28-FEB-2003 (Rel. 41, Last Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 05-JUL-2004 (Rel. 44, Last annotation update)
 DE MLN64-like protein (Fragment).
 GN Name=MLN64;
 OS Salvelinus fontinalis (Brook trout) (Brook char).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 OC Protacanthopterygii; Salmoniformes; Salmonidae; Salvelinus.
 OC NCBI_TaxID=8038;
 OX 1)
 RN
 RP SEQUENCE FROM N.A.

RA Goetz F.W.;
 RT "Cloning and characterization of trout MLN64.";
 RL Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
 CC -1- FUNCTION: Binds and transports cholesterol. Promotes
 CC sterologenesis (by similarity).
 CC -1- SIMILARITY: Contains 1 START domain.
 CC
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration
 CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
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 CC use by non-profit institutions as long as its content is in no way
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 CC entities requires a license agreement (See <http://www.isb-sib.ch/announce/>
 CC or send an email to license@isb-sib.ch).
 CC
 DR EMBL; AF284379; AA082881.1; -.
 DR InterPro; IPR000799; STAR.
 DR InterPro; IPR002913; START.
 DR Pfam; PF01852; START; 1.
 DR PRINTS; PR00978; STARPROTEIN.
 DR SMART; SM00234; START; 1.
 DR PROSITE; PSS0848; START; 1.
 DR Lipid transport; Lipid-binding; Steroidogenesis; Transport.
 KW NON TER 1
 FT DOMAIN 1 292 START.
 SQ SEQUENCE 294 AA; 32807 MW; E1C3F2CB32C2BA91 CRC64;
 Query Match 8.7%; Score 104.5; DB 1; Length 294;
 Best Local Similarity 66.7%; Pred. No. 0.39;
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 QY 186 LLIVQASERAAI-PGSLSDGQFYSPPESEAGSEE 220
 DB 33 LAAVNAASERAAPIYRAVSEGFYSPPESLAAGEE 68

Search completed: May 17, 2005, 10:24:41
 Job time : 106 secs

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OM protein - protein search, using sw model

Run on: May 17, 2005, 10:15:40 ; Search time 17 seconds
(Without alignments)
1324.395 Million cell updates/sec

Title: US-10-063-518-14
Perfect score: 1195
Sequence: 1 MNHLPEDEMNALTGSSQSHA.....EAGSEAEKQDEKPLEL 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :
1: p1r1:*
2: p1r2:*
3: p1r3:*
4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	664	55.6	445	2	138027
2	204	17.1	478	2	116170
3	102.5	8.6	348	2	H90281
4	93.5	7.8	424	2	D75080
5	90	7.5	1911	2	T43048
6	86.5	7.2	767	2	T21969
7	85.5	7.2	366	2	B81299
8	85.5	7.2	438	2	A57219
9	85	7.1	448	2	G70172
10	84.5	7.1	471	2	A41680
11	83.5	7.0	352	2	H97002
12	83	6.9	291	2	AE0302
13	83	6.9	590	1	S34960
14	82.5	6.9	186	2	B29835
15	82.5	6.9	239	1	C64227
16	82.5	6.9	341	2	S51265
17	82.5	6.9	406	2	T43130
18	82.5	6.9	891	2	T37397
19	82	6.9	589	2	T52070
20	82	6.9	589	2	A36983
21	82	6.9	1466	2	T30566
22	81	6.8	385	2	B84447
23	81	6.8	529	2	T23130
24	81	6.8	532	2	S46831
25	80.5	6.7	156	2	T84498
26	80.5	6.7	322	2	T45568
27	80.5	6.7	396	2	T50229
28	80.5	6.7	417	2	C44038
29	80.5	6.7	463	2	AE1155

30	80.5	6.7	536	2	A71491	probable integral
31	80.5	6.7	738	2	S63056	probable membrane
32	80.5	6.7	644	2	S10659	membrane protein t
33	80.5	6.7	891	1	MNV238	major core protein
34	80.5	6.7	891	1	MNV238	major core protein
35	80.5	6.7	1780	2	A85045	probable glycan sy
36	80	6.7	103	2	G75513	conserved hypotnet
37	80	6.7	290	2	D89898	hypothetical prote
38	80	6.7	309	2	S59140	RTM1 protein - Yea
39	80	6.7	388	2	H71115	hypothetical prote
40	80	6.7	1339	2	A84683	probable SNF2 subf
41	79.5	6.7	463	2	AH1513	amino acid transpo
42	79.5	6.7	491	1	EDBERC	immediate-early pr
43	78.5	6.6	239	2	S73812	hypothetical prote
44	78.5	6.6	269	2	AF1532	spermidine/putresc
45	78.5	6.6	358	2	F64136	rtfd protein homol
46	78.5	6.6	471	2	S11280	serotonin receptor
47	78.5	6.6	678	2	S44925	IB3/5-polyepitide
48	78	6.5	245	2	JC5346	cd22 protein - Clo
49	78	6.5	259	2	F83825	hypothetical prote
50	78	6.5	382	2	E97157	stage III sporulat
51	78	6.5	471	2	B64089	undecaprenyl phosp
52	78	6.5	1297	2	T39287	hypothetical prote
53	78	6.5	2136	2	A05037	hypothetical prote
54	77.5	6.5	269	2	AH1175	spermidine/putresc
55	77.5	6.5	299	2	AE0461	conserved membrane
56	77.5	6.5	327	2	F82904	ABC transporter (p
57	77.5	6.5	328	2	F84130	hypothetical prote
58	77.5	6.5	338	2	T39159	NADH2 dehydrogenas
59	77.5	6.5	440	2	T11319	sodium- and chlori
60	77.5	6.5	491	2	B69499	probable colanic b
61	77.5	6.5	512	2	AC3399	NADH2 dehydrogenas
62	77.5	6.5	734	1	DERZM5	ALL protein - var
63	77.5	6.5	892	2	H72164	hypothetical prote
64	77.5	6.5	892	2	T28552	hypothetical prote
65	77.5	6.5	892	2	B36849	multidrug resistan
66	77.5	6.5	1784	2	T43167	hypothetical prote
67	77	6.4	332	2	T23307	hypothetical prote
68	77	6.4	559	2	C87307	hypothetical prote
69	77	6.4	590	1	QOUTC5	NADH2 dehydrogenas
70	77	6.4	650	2	A90072	hypothetical prote
71	77	6.4	991	2	T01377	hypothetical prote
72	77	6.4	1025	2	T18376	multidrug resistan
73	77	6.4	1117	2	C85018	hypothetical prote
74	77	6.4	1500	2	G84922	hypothetical prote
75	76.5	6.4	278	2	B85807	probable tail fibre
76	76.5	6.4	278	2	H90958	probable sugar ABC
77	76.5	6.4	282	2	H95869	hypothetical prote
78	76.5	6.4	352	2	T25170	hypothetical prote
79	76.5	6.4	352	2	AF0692	probable membrane
80	76.5	6.4	494	2	JC5919	potassium channel
81	76.5	6.4	538	2	B81435	probable iron-upca
82	76.5	6.4	589	2	A71918	probable secretion
83	76.5	6.4	646	2	T41545	hypothetical trans
84	76	6.4	342	2	T11476	NADH2 dehydrogenas
85	76	6.4	402	2	T24184	hypothetical prote
86	76	6.4	669	2	T48466	hypothetical prote
87	76	6.4	1402	2	T24664	hypothetical prote
88	76	6.4	1450	2	JC6139	cyclic fibrosis tr
89	76	6.4	1783	2	T37258	probable voltage id
90	76	6.4	1917	2	C88728	protein C48A7.1 (I
91	75.5	6.3	156	2	T62107	melatonin receptor
92	75.5	6.3	263	2	G95198	hypothetical prote
93	75.5	6.3	263	2	C98085	hypothetical prote
94	75.5	6.3	339	2	B82211	conserved membrane
95	75.5	6.3	352	2	H64919	hypothetical prote
96	75.5	6.3	352	2	G85769	hypothetical prote
97	75.5	6.3	352	2	C90921	hypothetical prote
98	75.5	6.3	415	2	F91209	low affinity trypt
99	75.5	6.3	415	2	A86056	low affinity trypt
100	75.5	6.3	415	2	A39412	tryptophan transpo
101	75.5	6.3	471	2	S40689	5-hydroxytryptamin
102	75.5	6.3	498	2	T11039	NADH2 dehydrogenas

103	75.5	6.3	593	2	H64594	multidrug resistan	176	72.5	6.1	325	2	H86670	hypothetical prote
104	75.5	6.3	708	2	T29669	hypothetical prote	177	72.5	6.1	336	2	C88951	protein C38C3.2 [1
105	75.5	6.3	775	2	T52107	atlon channel prot	178	72.5	6.1	389	2	A55493	oxytocin receptor
106	75.5	6.3	1142	2	T39103	probable negativ	179	72.5	6.1	428	2	AF0173	probable parquat-
107	75	6.3	249	2	G64470	bullate/chitosulat	180	72.5	6.1	499	2	H70453	vinience factor M
108	75	6.3	274	2	A82509	probable phosphat	181	72.5	6.1	513	2	S47631	pituitary adenylat
109	75	6.3	330	2	B71163	gamma-oligopept	182	72.5	6.1	522	2	T29705	hypothetical prote
110	75	6.3	473	2	A38627	probable oligopept	183	72.5	6.1	635	2	T23465	hypothetical prote
111	75	6.3	526	2	T45850	hypothetical prote	184	72.5	6.1	718	2	S57913	probable transloca
112	75	6.3	649	2	G69810	anion-binding prot	185	72.5	6.1	749	2	C84508	probable cap-bindi
113	75	6.3	753	2	H90124	hypothetical prote	186	72.5	6.1	1539	2	T30037	hypothetical prote
114	75	6.3	2248	1	D42068	adenylate cyclase	187	72	6.0	279	2	T21099	hypothetical prote
115	74.5	6.2	276	2	A95881	probable trehalose	188	72	6.0	306	2	AB1156	hypothetical prote
116	74.5	6.2	335	2	H73420	oligopeptide ABC c	189	72	6.0	339	2	G97199	probable permease
117	74.5	6.2	355	2	JC4304	orphan G protein-c	190	72	6.0	377	2	T27805	hypothetical prote
118	74.5	6.2	473	2	A34863	serotonin receptor	191	72	6.0	379	2	T11349	ubiquinol-cytochro
119	74.5	6.2	473	2	B84143	Na+/H+ antiporter	192	72	6.0	415	1	MMAD52	late L1 52K protei
120	74.5	6.2	500	2	T14826	transcription init	193	72	6.0	415	1	MMAD65	glycosyl hydrolase
121	74.5	6.2	574	2	T05964	probable low-affin	194	72	6.0	453	2	T39155	conserved hypochet
122	74.5	6.2	618	1	S38004	hypothetical prote	195	72	6.0	453	2	D89760	hypothetical prote
123	74.5	6.2	1808	1	T47792	hypothetical prote	196	72	6.0	479	2	S64587	probable cytochrom
124	74	6.2	231	1	G69540	cobalamin (5'-phos	197	72	6.0	497	2	G96611	hypothetical prote
125	74	6.2	231	1	B69422	quinone-reactive N	198	72	6.0	514	2	T15338	hypothetical prote
126	74	6.2	281	1	S26018	NMDH2 dehydrogenas	199	72	6.0	534	2	T42660	hypothetical prote
127	74	6.2	286	1	S73424	spermidine/putresc	200	72	6.0	600	2	T39673	hypothetical prote
128	74	6.2	312	2	C72547	probable aspartate	201	72	6.0	630	2	T07966	probable ethylene
129	74	6.2	312	2	H86732	hypothetical prote	202	72	6.0	1038	2	S37854	hypothetical prote
130	74	6.2	349	2	JC6311	interferon recepto	203	72	6.0	1094	2	S22573	DNA-directed DNA p
131	74	6.2	350	2	I38848	Mel-1a melanotin r	204	72	6.0	1113	2	T20140	hypothetical prote
132	74	6.2	396	2	H89869	hypothetical prote	205	72	6.0	1220	2	T18291	patched protein -
133	74	6.2	442	2	C86859	transmembrane effi	206	72	6.0	1275	2	UU0092	crp protein - fru1
134	74	6.2	449	2	S02011	serotonin receptor	207	72	6.0	1282	2	T30804	p-glycoprotein 6 -
135	74	6.2	475	2	T26137	probable amino aci	208	72	6.0	210	2	SM2050	cytochrome-c oxida
136	74	6.2	485	2	T24115	hypothetical prote	209	71.5	6.0	225	1	MMH68	B1 membrane glycop
137	74	6.2	487	1	C71417	cytochrome P450 d1	210	71.5	6.0	237	2	H70975	hypothetical prote
138	74	6.2	493	2	UC7378	L-lysine 6-aminotr	211	71.5	6.0	246	2	AG3544	flagellar biosynth
139	74	6.2	1123	2	T51517	telomerase reverse	212	71.5	6.0	301	2	F86647	hypothetical prote
140	73.5	6.2	153	2	E95845	conserved hypochet	213	71.5	6.0	311	2	F90084	hypothetical prote
141	73.5	6.2	192	2	A84727	hypothetical prote	214	71.5	6.0	345	2	T33706	hypothetical prote
142	73.5	6.2	216	2	G70474	hypothetical prote	215	71.5	6.0	348	2	D82252	snfD-related prote
143	73.5	6.2	318	2	S76713	hypothetical prote	216	71.5	6.0	355	2	AB3516	sensory transducti
144	73.5	6.2	338	2	I40448	conserved hypochet	217	71.5	6.0	352	2	S48689	prostaglandin E(2)
145	73.5	6.2	379	2	S58448	ubiquinol-cytochro	218	71.5	6.0	366	2	S51280	EP3-alpha receptor
146	73.5	6.2	384	2	AF0636	glucans biosynthes	219	71.5	6.0	366	2	I46469	Mel-1a melanotin r
147	73.5	6.2	385	1	S01511	ubiquinol-cytochro	220	71.5	6.0	383	2	T11776	ubiquinol-cytochro
148	73.5	6.2	385	2	A69804	ABC transporter (A	221	71.5	6.0	393	2	T38194	hypothetical prote
149	73.5	6.2	413	2	AD1738	similar to multidr	222	71.5	6.0	386	1	S34043	oxytocin receptor
150	73.5	6.2	442	2	C96672	hypothetical prote	223	71.5	6.0	390	2	S66497	isotocin receptor
151	73.5	6.2	491	1	EDBEH5	immediate-early pr	224	71.5	6.0	435	2	AD1340	maltoedextrin ABC-c
152	73.5	6.2	634	2	F82623	potaesium uptake p	225	71.5	6.0	435	2	AB1711	maltoedextrin ABC-c
153	73.5	6.2	637	2	H83945	DNA mismatch repai	226	71.5	6.0	471	2	PS0154	125K surface anti
154	73.5	6.2	640	2	B32935	hypothetical prote	227	71.5	6.0	510	2	T10124	hexose transport p
155	73.5	6.2	731	2	T31914	hypothetical prote	228	71.5	6.0	524	2	T02499	hypothetical prote
156	73.5	6.2	1095	2	E96744	probable oligopept	229	71.5	6.0	603	2	H90061	hypothetical prote
157	73.5	6.2	1174	2	A39927	RNA-directed RNA p	230	71.5	6.0	651	2	T46050	hypothetical prote
158	73	6.2	114	2	F71925	cag island protein	231	71.5	6.0	669	2	D64137	bet1 protein homol
159	73	6.1	282	2	S26030	NMDH2 dehydrogenas	232	71.5	6.0	670	2	A49580	meditex transport
160	73	6.1	339	2	T15560	hypothetical prote	233	71.5	6.0	823	2	T34472	hypothetical prote
161	73	6.1	450	1	M2B8E4	49.2K membrane pro	234	71.5	6.0	1407	2	B42239	adenylate cyclase
162	73	6.1	453	2	T30985	hypothetical prote	235	71.5	6.0	310	1	S18030	genome polyprote
163	73	6.1	553	2	A71823	hypothetical prote	236	71	5.9	114	2	H64586	cag pathogenicity
164	73	6.1	788	2	G89901	hypothetical prote	237	71	5.9	225	1	MMHAI1	B1 membrane glycop
165	73	6.1	971	2	T00268	hypothetical prote	238	71	5.9	250	2	A82367	conserved hypochet
166	73	6.1	1075	2	B96508	hypothetical prote	239	71	5.9	258	2	AB1355	probable processin
167	73	6.1	6805	2	S20901	titin - rabbit (fr	240	71	5.9	290	2	S33443	chlorophyll a/b-bi
168	72.5	6.1	209	2	S72929	hypothetical prote	241	71	5.9	339	2	T16745	hypothetical prote
169	72.5	6.1	222	2	B85866	probable transport	242	71	5.9	345	2	T12372	NMDH2 dehydrogenas
170	72.5	6.1	222	2	B91022	probable transport	243	71	5.9	345	2	T25561	hypothetical prote
171	72.5	6.1	222	2	H64596	hypothetical prote	244	71	5.9	361	2	C90603	hypothetical prote
172	72.5	6.1	255	2	A60944	ubiquinol-cytochro	245	71	5.9	391	2	F86759	hypothetical prote
173	72.5	6.1	291	2	T02986	chlorophyll a/b-bi	246	71	5.9	416	2	E87286	3-deoxy-D-manno-oc
174	72.5	6.1	307	2	A86596	conserved hypochet	247	71	5.9	423	2	AF1335	transcription regu
175	72.5	6.1	315	2	H96598	protein F20M2.8 [1	248	71	5.9	471	2	A43956	serotonin receptor

249	71	5.9	546	2	S48932	322	69.5	5.8	285	2	F70194	hypothetical prote
250	71	5.9	563	2	T38766	323	69.5	5.8	321	2	S59388	probable membrane
251	71	5.9	576	2	T22509	324	69.5	5.8	339	2	A97736	hypothetical prote
252	71	5.9	620	2	A58932	325	69.5	5.8	347	2	G90444	hypothetical prote
253	71	5.9	676	2	E96725	326	69.5	5.8	354	2	I58186	probable G protein
254	71	5.9	788	2	E71813	327	69.5	5.8	361	2	A53216	prostaglandin E2 r
255	71	5.9	913	2	T52485	328	69.5	5.8	362	2	S36766	prostaglandin E re
256	71	5.9	2437	2	T18482	329	69.5	5.8	384	2	S62758	ubiquinol-cytochro
257	70.5	5.9	203	1	T31684	330	69.5	5.8	385	2	S36765	prostaglandin E re
258	70.5	5.9	266	2	H98208	331	69.5	5.8	387	2	S36767	prostaglandin E re
259	70.5	5.9	266	2	A13077	332	69.5	5.8	394	2	T32561	hypothetical prote
260	70.5	5.9	266	2	A13077	333	69.5	5.8	400	2	AG1208	cell-division prot
261	70.5	5.9	279	2	T41414	334	69.5	5.8	402	2	S51791	Drosophila translo
262	70.5	5.9	291	2	S22041	335	69.5	5.8	405	2	E90986	probable colanic a
263	70.5	5.9	340	2	S76294	336	69.5	5.8	405	2	H85831	probable colanic a
264	70.5	5.9	352	2	B90537	337	69.5	5.8	405	2	G64971	putative colanic a
265	70.5	5.9	365	2	I38748	338	69.5	5.8	411	2	B53216	prostaglandin E2 r
266	70.5	5.9	374	2	S51315	339	69.5	5.8	417	2	S36764	prostaglandin E re
267	70.5	5.9	374	2	I38747	340	69.5	5.8	421	2	G72300	conserved hypothet
268	70.5	5.9	374	2	S51317	341	69.5	5.8	436	2	T44832	probable emulsan r
269	70.5	5.9	388	2	S51316	342	69.5	5.8	453	2	D98003	conserved hypothet
270	70.5	5.9	388	2	I38750	343	69.5	5.8	477	2	T25798	hypothetical prote
271	70.5	5.9	389	2	S71336	344	69.5	5.8	490	2	E82740	C4-dicarboxylate t
272	70.5	5.9	390	2	S43375	345	69.5	5.8	503	2	C86250	hypothetical prote
273	70.5	5.9	390	2	S51313	346	69.5	5.8	507	2	T50054	probable transport
274	70.5	5.9	393	2	S51318	347	69.5	5.8	515	2	E86534	ADP/ATP translocas
275	70.5	5.9	423	1	E71065	348	69.5	5.8	547	2	G86581	integral membrane
276	70.5	5.9	425	2	S51319	349	69.5	5.8	547	2	F72042	integral membrane
277	70.5	5.9	426	2	AG3600	350	69.5	5.8	557	2	UW0089	organic cation tra
278	70.5	5.9	432	2	B64638	351	69.5	5.8	557	2	AC2137	ABC transporter AT
279	70.5	5.9	521	2	E64181	352	69.5	5.8	570	2	B96776	hypothetical prote
280	70.5	5.9	548	2	A81650	353	69.5	5.8	577	2	D97337	mismatch repair pr
281	70.5	5.9	556	2	T16790	354	69.5	5.8	579	2	AG1412	DNA polymerase III
282	70.5	5.9	574	2	S45754	355	69.5	5.8	579	2	AF1788	gamma-aminobutyric
283	70.5	5.9	598	2	F46027	356	69.5	5.8	599	2	S11073	gamma-aminobutyric
284	70.5	5.9	599	1	ACR1GT	357	69.5	5.8	604	2	T31042	hypothetical prote
285	70.5	5.9	700	2	T10566	358	69.5	5.8	607	2	F84525	Mutator-like trans
286	70.5	5.9	766	2	T48463	359	69.5	5.8	616	2	E84463	Mutator-like trans
287	70.5	5.9	1026	2	T18220	360	69.5	5.8	877	2	S58824	probable membrane
288	70.5	5.9	1583	2	F97846	361	69.5	5.8	881	2	S46633	probable membrane
289	70.5	5.9	1787	2	T20160	362	69.5	5.8	1704	2	A59188	ATP-binding casaset
290	70.5	5.9	5138	2	B96695	363	69.5	5.8	1704	2	S71363	probable ATP-bindl
291	70	5.9	189	2	T51847	364	69.5	5.8	1778	2	JT0382	apolipoprotein B -
292	70	5.9	199	2	T08902	365	69.5	5.8	2629	2	T16569	hypothetical prote
293	70	5.9	213	2	F86310	366	69.5	5.8	7829	2	T15789	hypothetical prote
294	70	5.9	256	2	T13597	367	69.5	5.8	169	2	E83941	hypothetical prote
295	70	5.9	287	2	T52317	368	69.5	5.8	195	2	A96998	CDP-diglyceride sy
296	70	5.9	292	2	H64244	369	69.5	5.8	244	2	H96934	uncharacterized me
297	70	5.9	307	2	E95010	370	69.5	5.8	256	2	G64145	hypothetical prote
298	70	5.9	307	2	B97882	371	69.5	5.8	261	2	T07481	hypothetical prote
299	70	5.9	330	2	T30981	372	69.5	5.8	273	2	F83805	hypothetical prote
300	70	5.9	333	2	I38974	373	69.5	5.8	273	2	C71707	hypothetical prote
301	70	5.9	371	2	T46421	374	69.5	5.8	289	2	S72554	melatonin receptor
302	70	5.9	388	2	A55597	375	69.5	5.8	291	2	D96002	probable sugar upt
303	70	5.9	416	2	A85112	376	69.5	5.8	300	2	T32702	hypothetical prote
304	70	5.9	418	2	T08882	377	69.5	5.8	338	2	A99979	hypothetical prote
305	70	5.9	420	2	E72357	378	69.5	5.8	339	2	B69436	LSU ribosomal prot
306	70	5.9	427	2	T01905	379	69.5	5.8	345	2	AH1514	hypothetical prote
307	70	5.9	437	2	C91261	380	69.5	5.8	351	2	AD0273	probable integral
308	70	5.9	438	2	E86101	381	69.5	5.8	379	2	S58447	ubiquinol-cytochro
309	70	5.9	437	2	AP3215	382	69.5	5.8	382	2	A13175	conserved hypothet
310	70	5.9	450	2	T42595	383	69.5	5.8	383	2	D71424	hypothetical prote
311	70	5.9	494	2	B89827	384	69.5	5.8	388	2	T66544	O-antigen polymera
312	70	5.9	532	2	T49467	385	69.5	5.8	436	2	T11268	NADH2 dehydrogenas
313	70	5.9	551	2	A87019	386	69.5	5.8	437	2	A42384	glutamate-aspartat
314	70	5.9	554	2	T27878	387	69.5	5.8	443	2	T19512	hypothetical prote
315	70	5.9	558	2	H72565	388	69.5	5.8	478	2	S25821	transposase - Bac1
316	70	5.9	675	2	T22323	389	69.5	5.8	478	2	T33985	hypothetical prote
317	70	5.9	735	2	S46830	390	69.5	5.8	508	2	E96804	probable thiorodox
318	70	5.9	963	2	T26022	391	69.5	5.8	523	2	T11916	NADH2 dehydrogenas
319	70	5.9	1930	2	F86200	392	69.5	5.8	540	2	T24675	hypothetical prote
320	69.5	5.8	133	1	MN1HHC	393	69.5	5.8	549	2	E70784	cytochrome b homol
321	69.5	5.8	206	2	S76279	394	69.5	5.8	579	2	A64100	inner membrane cop

395	69	5.8	599	2	G90476	probable Na+/H+ an	468	68	5.7	426	2	C69631	conserved hypothe
396	600	5.8	600	2	T11889	NADH2 dehydrogenas	469	68	5.7	464	2	C70414	NADH2 dehydrogenas
397	69	5.8	637	2	H96592	probable multipep	470	68	5.7	473	2	H71044	hypothetical prote
398	659	5.8	659	2	D84633	probable multipep	471	68	5.7	475	2	B83450	cytochrome-c oxida
399	69	5.8	791	2	T12455	hypothetical prote	472	68	5.7	477	2	H91123	probable oxidoredu
400	69	5.8	802	2	JH0595	potassium channel	473	68	5.7	477	2	G85968	probable oxidoredu
401	69	5.8	863	2	H84450	hypothetical prote	474	68	5.7	477	2	C65096	hypothetical 52.1
402	69	5.8	933	2	AD3309	hypothetical membr	475	68	5.7	488	2	A53572	prostaglandin 52 r
403	69	5.8	1058	2	T30580	P-type ATPase - s1	476	68	5.7	502	1	I30010	NADH2 dehydrogenas
404	69	5.8	1344	2	T34188	myb-binding protei	477	68	5.7	519	2	T39918	probable acetyl-co
405	69	5.8	1392	2	T01908	hypothetical prote	478	68	5.7	542	2	A69261	probable acid-CoA
406	69	5.8	1515	2	T04204	hypothetical prote	479	68	5.7	542	2	B81910	probable ABC-trans
407	69	5.8	3010	1	A45573	genome polypeptid	480	68	5.7	542	2	B81105	ABC transporter, A
408	69	5.7	225	2	AE0371	probable carboxype	481	68	5.7	620	2	T119907	hypothetical prote
409	69	5.7	237	2	T25877	hypothetical prote	482	68	5.7	664	2	C84869	probable receptor
410	69	5.7	238	2	T04280	hypothetical prote	483	68	5.7	718	2	B83718	hypothetical prote
411	69	5.7	260	2	H75428	hypothetical prote	484	68	5.7	804	2	T49975	hypothetical prote
412	69	5.7	262	2	AG1830	hypothetical prote	485	68	5.7	836	2	T18460	hypothetical prote
413	69	5.7	265	2	A13428	O-antigen export s	486	68	5.7	859	2	S69700	hypothetical prote
414	69	5.7	285	2	B86835	maltoase export s	487	68	5.7	871	2	H72597	hypothetical prote
415	69	5.7	297	2	S74335	carbon dioxide con	488	68	5.7	1429	2	T19422	hypothetical prote
416	69	5.7	304	2	AG3035	hypothetical prote	489	68	5.7	1878	2	B86189	hypothetical prote
417	69	5.7	304	2	D98250	probable sugar ABC	490	68	5.7	3010	1	GNMYTC	genome polypeptid
418	69	5.7	343	2	AC2129	iron(III) dicitrat	491	68	5.7	104	2	T36801	hypothetical prote
419	69	5.7	359	2	B59105	hypothetical prote	492	68	5.7	200	2	H72295	conserved hypothe
420	69	5.7	362	2	D72424	oligopeptide ABC t	493	68	5.7	273	2	A97700	hypothetical prote
421	69	5.7	377	1	J02337	omega-3 fatty acid	494	68	5.7	288	2	F72219	conserved hypothe
422	69	5.7	383	2	I53870	Bdg-1 orphan recep	495	68	5.7	320	2	T23674	hypothetical prote
423	69	5.7	391	2	H81265	probable transmem	496	68	5.7	323	1	QOBRD3	HRF3 protein - hu
424	69	5.7	395	2	B83774	hypothetical prote	497	68	5.7	348	2	T12591	NADH2 dehydrogenas
425	69	5.7	395	2	B83774	hypothetical prote	498	68	5.7	348	2	T12591	G protein-coupled
426	69	5.7	395	2	AH3097	conserved hypothe	499	68	5.7	362	2	C88086	protein T11P1.1 [i
427	69	5.7	419	2	AG1660	multidrug resistan	500	68	5.7	387	2	T24581	hypothetical prote
428	69	5.7	420	2	I51666	Mel-1c receptor su	501	68	5.7	397	2	A83999	mutants block spor
429	69	5.7	425	2	F97108	probable glycosyl	502	68	5.7	419	2	AH1288	multidrug resistan
430	69	5.7	430	2	S15308	hypothetical prote	503	68	5.7	439	2	H83599	sodium-dependent c
431	69	5.7	431	2	H72247	preproteins translo	504	68	5.7	450	2	G91219	TDP-Fuc4NAc lipid
432	69	5.7	444	2	A48260	corticoidliferin rec	505	68	5.7	450	2	A86066	TDP-Fuc4NAc lipid
433	69	5.7	445	2	E22845	hypothetical prote	506	68	5.7	450	2	F65183	4-alpha-1-fucosyl
434	69	5.7	479	2	T44326	hypothetical prote	507	68	5.7	452	2	G89870	hypothetical prote
435	69	5.7	480	2	B70446	hypothetical prote	508	68	5.7	459	2	JH0594	vasoactive intesti
436	69	5.7	488	2	T15941	hypothetical prote	509	68	5.7	483	2	G84113	hypothetical prote
437	69	5.7	490	2	G90574	NADH2 dehydrogenas	510	68	5.7	488	1	QXASMA	NADH2 dehydrogenas
438	69	5.7	502	2	S77331	probable cyclochrom	511	68	5.7	492	2	F64464	sodium-dependent n
439	69	5.7	512	2	T00605	pac2 protein - Yea	512	68	5.7	498	2	T48262	hypothetical prote
440	69	5.7	518	2	S50465	pac2 protein - Yea	513	68	5.7	515	2	E72089	ADP, ATP carrier p
441	69	5.7	525	2	JN0902	pituitary adenylat	514	68	5.7	516	2	H82973	choline transporte
442	69	5.7	542	2	S58102	hypothetical prote	515	68	5.7	566	2	I51368	gamma-aminobutyric
443	69	5.7	558	2	F64235	Na+ ATPase chain v	516	68	5.7	632	2	A71259	probable dicarboxy
444	69	5.7	634	2	C83530	potassium uptake p	517	68	5.7	676	1	WZV218	18 protein - vacc1
445	69	5.7	670	2	C86702	unknown protein [i	518	68	5.7	676	1	T37345	NPH-II, helicase -
446	69	5.7	724	2	H86427	cation-transportin	519	68	5.7	676	2	D42511	18R protein - vacc
447	69	5.7	788	2	G64707	probable membrane	520	68	5.7	676	2	F36843	ATP/GTP-binding pr
448	69	5.7	923	1	MMBY7C	probable copper-tr	521	68	5.7	676	2	T28500	hypothetical prote
449	69	5.7	1004	1	S55353	hypothetical prote	522	68	5.7	682	2	D72158	18R protein - vari
450	69	5.7	146	2	H75201	hypothetical prote	523	68	5.7	686	2	G82448	sensor histidine k
451	69	5.7	205	2	A64373	hypothetical prote	524	68	5.7	716	2	S30687	hypothetical prote
452	69	5.7	255	2	F39925	hypothetical prote	525	68	5.7	740	1	T02567	probable ATP-bindi
453	69	5.7	266	2	C95316	probable ABC trans	526	68	5.7	866	2	A54163	vacuolar ATPase (E
454	69	5.7	270	2	AE3627	maltoase transport	527	68	5.7	866	2	T20574	hypothetical prote
455	69	5.7	279	2	AG2165	bicarbonate transp	528	68	5.7	950	2	T15915	hypothetical prote
456	69	5.7	294	2	T41953	G protein-coupled	529	68	5.7	1159	2	T02866	hypothetical prote
457	69	5.7	294	2	AE0004	ribonuclease BN (E	530	68	5.7	1244	2	T19615	hypothetical prote
458	69	5.7	313	2	B38888	COI intiron 9 prote	531	68	5.7	1411	2	S48442	PDR1 protein - ye
459	69	5.7	355	2	A45177	chemokine (C-C) re	532	68	5.7	1753	2	S30855	hypothetical prote
460	69	5.7	360	2	T11067	ubiquinol-cytochro	533	68	5.7	2332	1	GNMYF	genome polypeptid
461	69	5.7	364	2	JC2115	prostaglandin E re	534	68	5.7	151	2	A72093	conserved hypothe
462	69	5.7	365	2	JN0693	ubiquitinol-cytochro	535	68	5.7	151	2	H86529	CT101 hypothetical
463	69	5.7	370	2	H90559	ubiquitinol-cytochro	536	68	5.7	159	2	S61040	probable membrane
464	69	5.7	379	2	S58450	ubiquitinol-cytochro	537	68	5.7	180	2	T49129	Xel69 (escapes X-1
465	69	5.7	393	2	AG0184	probable multidrug	538	68	5.7	203	2	D70150	hypothetical glycop
466	69	5.7	402	2	T41253	hypothetical wct5	539	68	5.7	225	1	MMHIB	El membrane glycop
467	69	5.7	417	2	T11387	NADH2 dehydrogenas	540	68	5.7	244	2	D70404	conserved hypothe

541	67	5.6	255	2	C90078	hypothetical prote	614	66.5	5.6	412	2	G89773	hypothetical prote
542	67	5.6	275	2	G98194	sugar ABC transpor	615	66.5	5.6	413	2	H95041	polyaccharide tra
543	67	5.6	275	2	AC3092	hypothetical prote	616	66.5	5.6	435	2	D98111	hypothetical prote
544	67	5.6	275	2	575698	hypothetical prote	617	66.5	5.6	435	2	G95246	maltoedectrin ABC t
545	67	5.6	276	2	F69307	conserved hypochet	618	66.5	5.6	452	2	B95135	MATE efflux family
546	67	5.6	276	2	S35270	DNA-damage repair	619	66.5	5.6	462	2	H71228	hypothetical prote
547	67	5.6	283	2	AE6959	rRNA-processing ri	620	66.5	5.6	488	2	G71969	cytochrome-c oxid
548	67	5.6	285	2	AE1024	hypothetical prote	621	66.5	5.6	490	2	D84998	low-affinity inorg
549	67	5.6	286	2	D64235	hypothetical prote	622	66.5	5.6	490	2	AA6391	CAMP receptor sub
550	67	5.6	314	2	D96703	hypothetical prote	623	66.5	5.6	491	2	AC1555	efflux transporter
551	67	5.6	317	2	D98260	inner membrane pro	624	66.5	5.6	493	2	A71875	hypothetical prote
552	67	5.6	336	2	A96997	ferriochrome transp	625	66.5	5.6	494	2	T32644	hypothetical prote
553	67	5.6	345	2	T21776	hypothetical prote	626	66.5	5.6	507	2	T27627	hypothetical prote
554	67	5.6	349	2	D84166	hypothetical prote	627	66.5	5.6	539	2	G83720	nickel transport s
555	67	5.6	350	2	C88987	protein C50H11.2 l	628	66.5	5.6	547	2	E91135	probable alkaline
556	67	5.6	352	2	T32314	hypothetical prote	629	66.5	5.6	547	2	H85980	probable alkaline
557	67	5.6	379	2	S58451	ubiquinol-cytochro	630	66.5	5.6	550	1	A48026	sterol O-acetyltras
558	67	5.6	379	2	S58449	ubiquinol-cytochro	631	66.5	5.6	582	2	C71424	hypothetical prote
559	67	5.6	396	1	C69291	pheromone shutdow	632	66.5	5.6	583	2	AI1510	C-terminal domain
560	67	5.6	407	2	E70309	hypothetical prote	633	66.5	5.6	588	2	T32430	hypothetical prote
561	67	5.6	411	2	E71500	probable amino aci	634	66.5	5.6	653	2	AG2696	cytochrome c-type
562	67	5.6	415	2	S74041	pyruvate synthase	635	66.5	5.6	663	2	G97478	cytochrome c-type
563	67	5.6	416	2	T64401	hypothetical prote	636	66.5	5.6	727	2	I16506	Na+/Cl(-)-depend
564	67	5.6	423	2	C95085	sodium-dependent c	637	66.5	5.6	727	2	S27043	neurotransmitter t
565	67	5.6	436	2	AC1021	proton glutamate s	638	66.5	5.6	782	2	S19876	genome polypeptide
566	67	5.6	441	2	F86279	hypothetical prote	639	66.5	5.6	862	2	B36786	hypothetical prote
567	67	5.6	446	2	G72287	hypothetical prote	640	66.5	5.6	889	2	T47311	hypothetical prote
568	67	5.6	446	2	A31986	glucose transpor	641	66.5	5.6	992	2	T27479	hypothetical prote
569	67	5.6	507	2	AB1707	glycine betaine tr	642	66.5	5.6	1014	2	T31433	Na+/Ca2+,K+-exchan
570	67	5.6	516	2	AB0665	probable membrane	643	66.5	5.6	1083	2	C88854	protein Fl1A10.3 l
571	67	5.6	646	2	JC7777	AMP binding casnet	644	66.5	5.6	1144	2	H81037	DNA polymerase III
572	67	5.6	717	2	T49238	hypothetical prote	645	66.5	5.6	1456	2	T15961	hypothetical prote
573	67	5.6	753	2	S58331	dolichyl-phosphate	646	66.5	5.6	1684	2	JW0057	gravin - human
574	67	5.6	769	2	F81415	DNA topoisomerase	647	66.5	5.6	1768	2	E85062	hypothetical prote
575	67	5.6	784	2	C82679	cell division prot	648	66.5	5.6	2151	1	S16449	genome polypeptide
576	67	5.6	787	2	PN0677	hypothetical prote	649	66.5	5.6	2285	1	G02434	DNA-directed DNA p
577	67	5.6	798	2	T34248	hypothetical prote	650	66.5	5.6	2833	2	AA3360	Inositol 1,4,5-tri
578	67	5.6	814	2	T05537	probable serine/th	651	66.5	5.6	3011	1	GNWVC3	genome polypeptide
579	67	5.6	823	2	T35280	probable integral	652	66.5	5.5	93	2	S28759	NMDH2 dehydrogen
580	67	5.6	880	2	D69427	conserved hypochet	653	66.5	5.5	130	2	D83820	diacylglycerol kin
581	67	5.6	891	2	B82495	probable NADH dehy	654	66.5	5.5	209	2	A89801	conserved hypochet
582	67	5.6	900	2	B69631	galactosamine-cont	655	66.5	5.5	276	2	H96816	hypothetical prote
583	67	5.6	1175	2	S39951	chitin synthase (E	656	66.5	5.5	279	2	SA2125	hypothetical prote
584	67	5.6	1242	1	D3BEC1	DNA-directed DNA p	657	66.5	5.5	285	2	D87447	sulfate ABC transp
585	67	5.6	1333	2	S63403	probable membrane	658	66.5	5.5	302	2	A99074	hypothetical prote
586	67	5.6	1511	2	A51151	pleiotropic drug r	659	66.5	5.5	305	2	I47040	sterol O-acetyltras
587	67	5.6	1575	2	G82905	conserved hypochet	660	66.5	5.5	317	1	B41671	iron transport pro
588	67	5.6	1879	2	T19481	hypothetical prote	661	66.5	5.5	318	2	B84291	hypothetical prote
589	67	5.6	1905	2	T18267	multidrug resistan	662	66.5	5.5	322	2	E71137	hypothetical prote
590	67	5.6	1993	2	T30982	sodium channel SCA	663	66.5	5.5	332	2	C97272	hypothetical prote
591	67	5.6	3010	1	GNWVC3	genome polypeptide	664	66.5	5.5	332	2	C97272	conserved membrane
592	67	5.6	153	1	G69847	conserved hypochet	665	66.5	5.5	370	1	I52315	G protein-coupled
593	67	5.6	203	2	T28732	hypothetical prote	666	66.5	5.5	379	1	S17405	ubiquinol-cytochro
594	67	5.6	204	2	C70506	hypothetical prote	667	66.5	5.5	379	1	S17405	ubiquinol-cytochro
595	67	5.6	218	2	C64586	cag pathogenicity	668	66.5	5.5	381	2	A35300	G protein-coupled
596	67	5.6	245	2	A81405	sec-independent pr	669	66.5	5.5	390	1	QO8RT9	protein UL33 - hum
597	67	5.6	263	2	A12384	hypothetical prote	670	66.5	5.5	397	2	T21154	hypothetical prote
598	67	5.6	268	2	A70417	hypothetical prote	671	66.5	5.5	397	2	T44477	hypothetical prote
599	67	5.6	272	2	A10075	probable permease	672	66.5	5.5	397	2	B70505	hypothetical prote
600	67	5.6	279	1	S56642	nitrate transpor	673	66.5	5.5	401	2	T44831	probable emulsan r
601	67	5.6	279	1	E70322	hypothetical prote	674	66.5	5.5	404	1	B64927	probable sugar tra
602	67	5.6	293	2	A84110	hypothetical prote	675	66.5	5.5	404	2	A85777	probable transport
603	67	5.6	294	2	S70876	sugar ABC transpor	676	66.5	5.5	404	2	E90928	probable transport
604	67	5.6	316	2	F81712	ABC transporter, p	677	66.5	5.5	411	2	H86539	CBS domain protein
605	67	5.6	333	2	S77103	hypothetical prote	678	66.5	5.5	412	2	A82444	Gdfer family prote
606	67	5.6	347	2	AD2201	hypothetical prote	679	66.5	5.5	418	2	T41027	hypothetical wfs
607	67	5.6	356	2	T20737	hypothetical prote	680	66.5	5.5	424	2	B72353	hypothetical prote
608	67	5.6	359	2	F90055	conserved hypochet	681	66.5	5.5	424	2	T07366	probable phosphact
609	67	5.6	367	2	S75936	hypothetical prote	682	66.5	5.5	436	2	T14816	hypothetical prote
610	67	5.6	380	2	G89786	hypothetical prote	683	66.5	5.5	437	2	T18633	hypothetical prote
611	67	5.6	384	1	I38890	dial specificity p	684	66.5	5.5	450	2	A37223	alpha-2b-adreneryl
612	67	5.6	389	2	E96516	Fl6N3.13 [imported	685	66.5	5.5	450	2	A38316	alpha-2-adreneryic
613	67	5.6	400	2	G00013	D3 dopamine recept	686	66.5	5.5	453	2	F86846	ABC transporter pe

687	66	5.5	483	2	S75369	hypothetical prote	760	65.5	5.5	561	2	S71189	Dwarf1 protein - A
688	66	5.5	484	2	T24238	hypothetical prote	761	65.5	5.5	575	2	AH1417	ABC transporter (A
689	66	5.5	486	2	E82940	hypothetical prote	762	65.5	5.5	578	2	T15736	hypothetical prote
690	66	5.5	508	2	C47677	hypothetical prote	763	65.5	5.5	583	2	AH1151	glycerophosphoryl
691	66	5.5	525	2	T28306	ORF MSV145 hypothe	764	65.5	5.5	590	2	C81316	probable sugar epi
692	66	5.5	527	2	G69635	PTS arbutin-like e	765	65.5	5.5	597	2	B82881	hypothetical prote
693	66	5.5	532	2	A90037	hypothetical prote	766	65.5	5.5	617	2	AB1167	phosphotransferase
694	66	5.5	546	2	A69890	hypothetical prote	767	65.5	5.5	618	2	AC1204	phosphotransferase
695	66	5.5	548	2	B87423	cytochrome-c oxida	768	65.5	5.5	642	2	H70331	ATP-dependent heli
696	66	5.5	552	2	S45886	hypothetical prote	769	65.5	5.5	718	2	A56851	Na+/myo-inositol c
697	66	5.5	565	2	S73707	Na(+) translocatin	770	65.5	5.5	720	2	H82198	RTX toxin transpor
698	66	5.5	570	2	S07744	NMDH2 dehydrogenas	771	65.5	5.5	721	2	AF1254	penicillin-binding
699	66	5.5	573	1	S33212	INDA1 protein - fu	772	65.5	5.5	740	2	S61568	probable membrane
700	66	5.5	573	2	AP1418	ABC transporter, A	773	65.5	5.5	860	1	QRHULD	LDL receptor precu
701	66	5.5	573	2	AH1793	ABC transporter, A	774	65.5	5.5	958	2	AC0204	cellulose 1,4-beta
702	66	5.5	619	2	T11314	NMDH2 dehydrogenas	775	65.5	5.5	1087	1	S41797	TYB protein - yea
703	66	5.5	632	2	T24405	hypothetical prote	776	65.5	5.5	1328	2	B22999	SRB8 protein - yea
704	66	5.5	654	2	A98350	hypothetical ABC t	777	65.5	5.5	1427	2	S74293	hypothetical prote
705	66	5.5	654	2	AF2932	hypothetical prote	778	65.5	5.5	1581	2	B71636	hypothetical prote
706	66	5.5	705	2	T48464	hypothetical prote	779	65.5	5.5	1635	2	T32452	probable membrane
707	66	5.5	721	2	A70764	probable glxX prot	780	65.5	5.4	126	2	AD0340	transcription regu
708	66	5.5	736	2	G01522	acidic 82 kDa prot	781	65.5	5.4	149	2	C69393	early K1B 21K prot
709	66	5.5	784	2	B90442	tricorn proteinase	782	65.5	5.4	176	1	Q1AD25	hypothetical prote
710	66	5.5	1039	2	S76747	hypothetical prote	783	65.5	5.4	196	2	S40728	E1 membrane glycop
711	66	5.5	1054	2	A61221	probable calcium t	784	65.5	5.4	225	1	MMIHIV	serotonin receptor
712	66	5.5	1359	2	T34036	hypothetical prote	785	65.5	5.4	247	2	I48149	hypothetical prote
713	66	5.5	1375	2	S48375	hypothetical prote	786	65.5	5.4	257	2	B75099	hypothetical prote
714	66	5.5	2599	2	P90608	ABC transporter pe	787	65.5	5.4	259	2	A47112	growth response pr
715	66	5.5	26926	1	I38344	titin, cardiac mus	788	65.5	5.4	271	2	E89950	nitrate transport
716	65.5	5.5	132	2	B97760	NMDH2 dehydrogenas	789	65.5	5.4	280	2	S75957	probable chlorophy
717	65.5	5.5	132	2	E70047	hypothetical prote	790	65.5	5.4	290	2	T07877	cytochrome c oxida
718	65.5	5.5	146	2	G69447	hypothetical prote	791	65.5	5.4	291	2	C97453	cytochrome c oxida
719	65.5	5.5	171	2	A13476	signal peptidase I	792	65.5	5.4	307	2	AB2671	branched-chain ami
720	65.5	5.5	197	2	T17106	hypothetical prote	793	65.5	5.4	313	2	B36125	lysophospholipase
721	65.5	5.5	210	2	S67771	endoplasmic reticu	794	65.5	5.4	313	2	A64084	hypothetical prote
722	65.5	5.5	252	2	T43100	signal sequence pe	795	65.5	5.4	322	2	S38091	hypothetical prote
723	65.5	5.5	290	2	F69456	phosphate ABC tran	796	65.5	5.4	335	2	H75068	dipeptide abc tran
724	65.5	5.5	297	2	F86839	hypothetical prote	797	65.5	5.4	330	2	H75029	hypothetical prote
725	65.5	5.5	297	2	F86839	hypothetical prote	798	65.5	5.4	335	2	H75029	NMDH2 dehydrogenas
726	65.5	5.5	301	2	T21308	hypothetical prote	799	65.5	5.4	338	2	S50339	conserved hypobhet
727	65.5	5.5	317	2	S23459	polysulfide reduct	800	65.5	5.4	344	2	AD1300	NMDH2 dehydrogenas
728	65.5	5.5	327	2	T36087	probable binding p	801	65.5	5.4	345	2	T12361	hypothetical prote
729	65.5	5.5	348	1	S36003	NMDH2 dehydrogenas	802	65.5	5.4	355	2	G70200	hypothetical prote
730	65.5	5.5	351	2	F82880	hypothetical ferrit	803	65.5	5.4	359	2	T15249	mannan endo-1,4-be
731	65.5	5.5	365	1	F69629	spore germination	804	65.5	5.4	362	2	H69785	ubiquitinol-cytochro
732	65.5	5.5	367	2	JC2056	prostaglandin B2 r	805	65.5	5.4	375	2	I38879	ubiquitinol-cytochro
733	65.5	5.5	379	2	S58456	ubiquitinol-cytochro	806	65.5	5.4	379	1	S17414	ubiquitinol-cytochro
734	65.5	5.5	379	2	T32778	hypothetical prote	807	65.5	5.4	379	2	S58461	ubiquitinol-cytochro
735	65.5	5.5	391	2	T32601	hypothetical prote	808	65.5	5.4	379	2	S58455	ubiquitinol-cytochro
736	65.5	5.5	394	2	AH0362	nucleoside permeas	809	65.5	5.4	380	1	D34285	ubiquitinol-cytochro
737	65.5	5.5	410	2	T11064	NMDH2 dehydrogenas	810	65.5	5.4	382	2	T11138	ubiquitinol-cytochro
738	65.5	5.5	423	2	E90569	conserved hypobhet	811	65.5	5.4	390	2	C84984	hypothetical prote
739	65.5	5.5	425	2	A97688	hypothetical 45.5K	812	65.5	5.4	415	2	T21532	hypothetical prote
740	65.5	5.5	425	2	AF2913	conserved hypobhet	813	65.5	5.4	438	2	B81410	probable integral
741	65.5	5.5	429	2	T32832	microfibril-associ	814	65.5	5.4	442	2	A83122	probable MRS trans
742	65.5	5.5	442	2	A42670	hypothetical prote	815	65.5	5.4	445	2	AD2358	glucosyltransferas
743	65.5	5.5	445	2	T38916	probable transcrip	816	65.5	5.4	457	2	T28334	Ser/Thr protein ki
744	65.5	5.5	449	2	H83629	probable dicarboxy	817	65.5	5.4	477	2	B88613	protein T27B9.5 [i
745	65.5	5.5	457	2	A75327	hypothetical prote	818	65.5	5.4	479	2	S54508	TRK system potassi
746	65.5	5.5	477	2	B75170	hypothetical prote	819	65.5	5.4	479	2	A69036	cytochrome-c oxida
747	65.5	5.5	480	2	A60043	endoplasmic reticu	820	65.5	5.4	481	2	E81050	probable sugar tra
748	65.5	5.5	487	2	A97928	type I site-specif	821	65.5	5.4	490	2	T14545	NMDH2 dehydrogenas
749	65.5	5.5	488	1	H64537	cytochrome-c oxida	822	65.5	5.4	492	2	S59107	hypothetical prote
750	65.5	5.5	491	2	G81295	cytochrome-c oxida	823	65.5	5.4	510	2	S55204	polyaccharide bio
751	65.5	5.5	491	2	AE1197	efflux transporter	824	65.5	5.4	511	2	H75097	probable membrane
752	65.5	5.5	495	2	A97022	probably membrane	825	65.5	5.4	513	2	T37180	hydrogenase 4 memb
753	65.5	5.5	500	2	G84706	hypothetical prote	826	65.5	5.4	526	2	D91047	conserved hypobhet
754	65.5	5.5	502	2	AD3395	NMDH2 dehydrogenas	827	65.5	5.4	530	2	B89771	hypothetical prote
755	65.5	5.5	502	2	T25669	hypothetical prote	828	65.5	5.4	535	2	A64697	hypothetical prote
756	65.5	5.5	518	2	A53207	probable folate tr	829	65.5	5.4	539	2	S55190	hypothetical prote
757	65.5	5.5	528	2	T34417	delayed rectifier	830	65.5	5.4	547	2	T31543	SNG1 protein - yea
758	65.5	5.5	544	2	B84825	probable ABC trans	831	65.5	5.4	547	2	S53920	hypothetical prote
759	65.5	5.5	545	2	B90460	hypothetical prote	832	65.5	5.4	576	2	T25375	

833	65	5.4	579	2	S61131	probable membrane
834	65	5.4	608	2	S65298	dicarboxylic amino
835	65	5.4	611	2	T21747	hypothetical prote
836	65	5.4	624	2	G82508	hypothetical prote
837	65	5.4	627	2	T11125	NMDH2 dehydrogenas
838	65	5.4	633	2	F84483	Mutator-like trans
839	65	5.4	638	2	D69957	conserved hypothet
840	65	5.4	643	2	P97787	sodium/pantothenat
841	65	5.4	676	2	A45515	diak-type molecula
842	65	5.4	684	2	F86394	protein T24P13.20
843	65	5.4	697	2	H84791	hypothetical prote
844	65	5.4	702	2	T13505	NMDH2 dehydrogenas
845	65	5.4	705	2	T04400	NMDH2 dehydrogenas
846	65	5.4	773	2	H96818	hypothetical prote
847	65	5.4	773	2	G83816	late competence op
848	65	5.4	808	2	T04459	hypothetical prote
849	65	5.4	861	2	S77086	hypothetical prote
850	65	5.4	927	2	T38518	ribonuclease II RN
851	65	5.4	931	2	F84637	probable plasma me
852	65	5.4	938	2	T01809	hypothetical prote
853	65	5.4	1089	2	C70522	probable mmp18 pro
854	65	5.4	1163	2	D64315	type I restriction
855	65	5.4	1176	2	S76370	sensory transducti
856	65	5.4	1232	2	I38496	anion exchanger 3
857	65	5.4	1421	2	T34225	hypothetical prote
858	65	5.4	5069	2	T17464	rifamycin polyketi
859	64.5	5.4	180	2	T41339	hypothetical prote
860	64.5	5.4	211	2	S35280	eac protein - phag
861	64.5	5.4	217	2	AE0395	probable amino aci
862	64.5	5.4	227	2	C69432	hypothetical prote
863	64.5	5.4	234	2	E96957	NAD superfamily hy
864	64.5	5.4	268	2	AF2470	potassium channel
865	64.5	5.4	271	2	B81384	prolipoprotein dia
866	64.5	5.4	275	2	T43119	hypothetical prote
867	64.5	5.4	293	2	D71517	probable metal tra
868	64.5	5.4	295	2	T32202	hypothetical prote
869	64.5	5.4	297	2	T27584	hypothetical prote
870	64.5	5.4	320	2	T23904	hypothetical prote
871	64.5	5.4	326	2	A86411	protein P3M18.6 [i
872	64.5	5.4	353	2	F64175	hypothetical prote
873	64.5	5.4	358	2	T22823	hypothetical prote
874	64.5	5.4	361	2	A86841	hypothetical prote
875	64.5	5.4	361	2	A40734	Pas (Pasover) pro
876	64.5	5.4	379	1	S43264	ubiquinol-cytochro
877	64.5	5.4	379	2	T11505	ubiquinol-cytochro
878	64.5	5.4	379	2	S58454	ubiquinol-cytochro
879	64.5	5.4	379	2	AS5077	ubiquinol-cytochro
880	64.5	5.4	381	1	CBMS	pituitary adenylat
881	64.5	5.4	381	2	S33449	hypothetical prote
882	64.5	5.4	385	2	H69154	phosphoglycerate k
883	64.5	5.4	398	2	H95057	phosphoglycerate k
884	64.5	5.4	398	2	A97927	LAG1 protein - Yea
885	64.5	5.4	400	2	G01977	rod shape-determin
886	64.5	5.4	411	2	S46800	ubiquinol-cytochro
887	64.5	5.4	416	2	AF1127	ubiquinol-cytochro
888	64.5	5.4	426	2	T45800	NMDH2 dehydrogenas
889	64.5	5.4	435	2	T11162	probable maltodext
890	64.5	5.4	435	2	AC0105	NMDH2 dehydrogenas
891	64.5	5.4	439	2	C22845	hypothetical prote
892	64.5	5.4	439	2	A84153	hypothetical prote
893	64.5	5.4	443	2	B26696	NMDH2 dehydrogenas
894	64.5	5.4	444	2	T11474	P44 hepatitis-aabo
895	64.5	5.4	444	2	A43676	microtubular aggre
896	64.5	5.4	444	2	S48218	dopamine receptor
897	64.5	5.4	446	1	DYRTD3	hypothetical prote
898	64.5	5.4	448	2	D85362	probable histidine
899	64.5	5.4	448	2	S57909	two-component sens
900	64.5	5.4	450	2	T23528	pituitary adenylat
901	64.5	5.4	451	2	D71045	transposase C - Ba
902	64.5	5.4	467	2	JN0616	glycinin chain Ala
903	64.5	5.4	478	2	C29051	glycinin Gl precur
904	64.5	5.4	495	1	FMSY22	
905	64.5	5.4	495	2	S10851	
906	64.5	5.4	495	2	S39061	pituitary adenylat
907	64.5	5.4	495	2	S36114	pituitary adenylat
908	64.5	5.4	512	2	H64664	probable membrane
909	64.5	5.4	521	2	A99549	amino acid permeas
910	64.5	5.4	523	2	S39060	pituitary adenylat
911	64.5	5.4	547	2	H65107	hypothetical 61.6
912	64.5	5.4	554	2	A56730	carl protein - Pod
913	64.5	5.4	555	2	B97812	virulence factor m
914	64.5	5.4	575	2	AB1793	ABC transporter (A
915	64.5	5.4	576	2	T05904	cytochrome P450 97
916	64.5	5.4	614	2	B89869	hypothetical prote
917	64.5	5.4	622	2	AC1236	acyltansiferase (t
918	64.5	5.4	638	1	QOBY2M	mRNA maturase b14
919	64.5	5.4	715	2	T26307	hypothetical prote
920	64.5	5.4	720	2	T47648	ABC transporter-11
921	64.5	5.4	721	2	AD1617	penicillin-binding
922	64.5	5.4	721	2	AE1491	hypothetical prote
923	64.5	5.4	735	2	AD0341	probable membrane
924	64.5	5.4	763	2	AD1070	phosphatidylglycer
925	64.5	5.4	801	2	A89862	Na+/H+ antiporter
926	64.5	5.4	803	2	H64568	histidine kinase -
927	64.5	5.4	889	2	T30715	probable major cor
928	64.5	5.4	979	2	A70848	probable membrane
929	64.5	5.4	1007	2	JC8066	138k protein - Tec
930	64.5	5.4	1114	2	JH0284	125k surface antiq
931	64.5	5.4	1146	2	B70723	probable mmp12 pr
932	64.5	5.4	1154	2	T48829	related to SRBP c
933	64.5	5.4	1465	2	S45628	DNA-directed DNA p
934	64.5	5.4	1465	2	S69688	hypothetical prote
935	64.5	5.4	1529	2	S66403	BSPI protein - Yea
936	64.5	5.4	1661	2	S64800	probable membrane
937	64.5	5.4	3033	1	GNWVJ8	genome polypeptid
938	64	5.4	202	2	A70041	conserved hypothet
939	64	5.4	209	2	G82359	conserved hypothet
940	64	5.4	253	2	JC5347	cdd3 protein - Clo
941	64	5.4	259	2	T12451	hypothetical prote
942	64	5.4	269	2	H69768	conserved hypothet
943	64	5.4	270	2	F89632	protein P136.3 [i
944	64	5.4	274	2	T50567	probable ABC-type
945	64	5.4	276	2	C70040	plant-metabolite d
946	64	5.4	276	2	S48358	probable membrane
947	64	5.4	281	2	C95932	probable sugar upt
948	64	5.4	283	2	D83009	probable permease
949	64	5.4	285	2	B83883	sugar transport sy
950	64	5.4	288	2	S36955	cytochrome-c oxida
951	64	5.4	330	2	T29675	hypothetical prote
952	64	5.4	342	2	A48258	dopamine receptor
953	64	5.4	347	2	T11248	NMDH2 dehydrogenas
954	64	5.4	351	2	S56716	protein kinase SPK
955	64	5.4	357	2	T20271	P16 protein - huma
956	64	5.4	359	2	H90587	hypothetical prote
957	64	5.4	369	2	S58452	ubiquinol-cytochro
958	64	5.4	370	1	S26031	ubiquinol-cytochro
959	64	5.4	376	2	G82656	ubiquinol-cytochro
960	64	5.4	378	2	D64181	ubiquinol-cytochro
961	64	5.4	379	1	CBBO	ubiquinol-cytochro
962	64	5.4	379	1	S17419	ubiquinol-cytochro
963	64	5.4	379	1	S26163	ubiquinol-cytochro
964	64	5.4	379	1	S43263	ubiquinol-cytochro
965	64	5.4	379	2	T11414	ubiquinol-cytochro
966	64	5.4	379	2	S58452	ubiquinol-cytochro
967	64	5.4	379	2	S58459	ubiquinol-cytochro
968	64	5.4	383	2	S55594	G protein-coupled
969	64	5.4	383	2	G64667	NA+/H+ antiporter
970	64	5.4	383	2	H71848	probable na+/h+ an
971	64	5.4	387	2	S74522	hypothetical prote
972	64	5.4	402	2	AD1417	drug-efflux transp
973	64	5.4	404	2	A97559	hypothetical prote
974	64	5.4	404	2	AE2779	acyltansiferase [i
975	64	5.4	409	2	S26021	NMDH2 dehydrogenas
976	64	5.4	411	2	A55610	corticotropin-rele
977	64	5.4	413	2	H81659	branched-chain ami
978	64	5.4	422	2	E84338	isocitrate dehydro

979	64	5.4	430	1	S32570	malC protein - Str	1052	63.5	5.3	327	2	S56162	MDCR15 protein - h
980	64	5.4	450	2	B40392	alpha-2-adrenergic	1053	63.5	5.3	328	2	D98215	oligopeptide ABC t
981	64	5.4	451	2	A36908	spore cortex penic	1054	63.5	5.3	328	2	T39824	septrin homolog - f
982	64	5.4	455	2	T31258	aromatic oxygenase	1055	63.5	5.3	334	2	B72393	oligopeptide ABC t
983	64	5.4	457	2	AF2975	aminotransferase,	1056	63.5	5.3	334	2	T41037	hypothetical prote
984	64	5.4	457	2	E98307	probable aminotran	1057	63.5	5.3	334	2	T27081	hypothetical prote
985	64	5.4	463	2	AC0281	probable amino aci	1058	63.5	5.3	342	2	A38908	spat0 protein - Sh
986	64	5.4	469	2	H90322	polysaccharide bio	1059	63.5	5.3	344	2	T34981	probable integral
987	64	5.4	492	2	B58931	NMDH2 dehydrogenas	1060	63.5	5.3	355	2	T15203	hypothetical prote
988	64	5.4	503	2	JC6627	cytochrome P450 3A	1061	63.5	5.3	359	2	D90172	hypothetical prote
989	64	5.4	511	2	T40334	hypothetical prote	1062	63.5	5.3	361	2	AE3071	hypothetical prote
990	64	5.4	527	2	AF5122	sodium- and chlori	1063	63.5	5.3	365	2	AB3494	oligopeptide trans
991	64	5.4	536	2	T36109	hypothetical prote	1064	63.5	5.3	372	2	S26667	G protein-coupled
992	64	5.4	544	2	C90406	conserved hypotnet	1065	63.5	5.3	377	2	B72275	probable aspartate
993	64	5.4	548	2	T13877	NMDH2 dehydrogenas	1066	63.5	5.3	380	1	CBRT	ubiquinol-cytochro
994	64	5.4	552	2	T52481	cytochrome-c oxida	1067	63.5	5.3	381	2	T11312	ubiquinol-cytochro
995	64	5.4	575	2	G75282	probable glutathio	1068	63.5	5.3	387	2	H88012	protein K1084.2 [i
996	64	5.4	586	1	A34400	ezrin [validated]	1069	63.5	5.3	389	2	G75133	hypothetical prote
997	64	5.4	598	2	T05130	hypothetical prote	1070	63.5	5.3	392	2	H71520	probable htn trans
998	64	5.4	602	2	C75120	hypothetical prote	1071	63.5	5.3	395	2	B81358	transmembrane tran
999	64	5.4	608	2	B69805	conserved hypotnet	1072	63.5	5.3	398	2	C71682	ubiquinol-cytochro
1000	64	5.4	609	2	G02640	polycystic kidney	1073	63.5	5.3	398	2	D81397	probable periplasm
1001	64	5.4	609	2	P70512	probable ATPase -	1074	63.5	5.3	399	2	B95080	cell division prot
1002	64	5.4	610	2	S37049	H+-exporting ATPas	1075	63.5	5.3	400	2	AG3016	phosphoglycerate k
1003	64	5.4	610	2	A69845	Na+/H+ antiporter	1076	63.5	5.3	401	2	T46306	hypothetical prote
1004	64	5.4	630	2	T47177	hypothetical prote	1077	63.5	5.3	404	1	LABECA	latent membrane pr
1005	64	5.4	634	2	C86677	DNA ligase (NAD) (1078	63.5	5.3	406	2	T19887	hypothetical prote
1006	64	5.4	651	2	T52460	hypothetical prote	1079	63.5	5.3	423	2	T04915	CDP-diacylglycerol
1007	64	5.4	657	2	T51779	non-phototropic hy	1080	63.5	5.3	423	2	G85255	CDP-diacylglycerol
1008	64	5.4	674	2	T50347	hypothetical prote	1081	63.5	5.3	426	2	A96268	phosphoglycerate k
1009	64	5.4	696	2	AB1566	hypothetical prote	1082	63.5	5.3	426	2	T33299	hypothetical prote
1010	64	5.4	748	2	T10651	hypothetical prote	1083	63.5	5.3	438	2	A82262	conserved hypotnet
1011	64	5.4	802	2	A87754	protein C43B11.11	1084	63.5	5.3	444	2	B85789	hypothetical prote
1012	64	5.4	838	2	H82939	conserved hypotnet	1085	63.5	5.3	445	2	T16025	hypothetical prote
1013	64	5.4	860	2	T37768	probable vacuolar	1086	63.5	5.3	447	2	P90940	hypothetical prote
1014	64	5.4	874	2	B86322	FAH1.8 protein -	1087	63.5	5.3	447	2	S52437	CDP-diacylglycerol
1015	64	5.4	896	2	AF1409	the two components	1088	63.5	5.3	450	2	B96738	hypothetical prote
1016	64	5.4	991	2	S57385	probable membrane	1089	63.5	5.3	452	2	T21118	hypothetical prote
1017	64	5.4	1024	1	RN208F	DNA-directed RNA P	1090	63.5	5.3	461	2	C97187	sugar transferase
1018	64	5.4	1078	2	T19745	hypothetical prote	1091	63.5	5.3	468	2	T48686	hypothetical prote
1019	64	5.4	1081	2	B81303	probable membrane	1092	63.5	5.3	485	2	H90562	mg2+ transport pro
1020	64	5.4	1227	2	A33638	erythrocyte anion	1093	63.5	5.3	487	2	B95059	hypothetical prote
1021	64	5.4	1385	2	T13415	hypothetical prote	1094	63.5	5.3	491	2	B64939	sugar transport re
1022	64	5.4	1462	1	DJHMAC	DNA-directed DNA P	1095	63.5	5.3	492	2	B90373	integral membrane
1023	64	5.4	1695	2	JE0084	voltage-gated sodi	1096	63.5	5.3	494	2	S76516	transporter like P
1024	64	5.4	2496	2	AF1616	secreted protein P	1097	63.5	5.3	498	2	T48385	transporter like P
1025	63.5	5.3	111	2	S43115	acidic ribosomal p	1098	63.5	5.3	498	2	T16190	NADH dehydrogenase
1026	63.5	5.3	123	2	G71682	NMDH2 dehydrogenas	1099	63.5	5.3	500	2	AF2325	hypothetical prote
1027	63.5	5.3	147	2	AH0495	probable membrane	1100	63.5	5.3	511	2	G90321	NADH dehydrogenase
1028	63.5	5.3	149	2	H70581	hypothetical prote	1101	63.5	5.3	512	1	A70201	hypothetical prote
1029	63.5	5.3	195	2	E71000	hypothetical prote	1102	63.5	5.3	525	2	A49601	virulence factor m
1030	63.5	5.3	214	2	C90191	conserved hypotnet	1103	63.5	5.3	537	2	G82873	nucleocapsid prote
1031	63.5	5.3	218	2	B71925	csg island protein	1104	63.5	5.3	540	1	I49454	conserved hypotnet
1032	63.5	5.3	218	2	T29205	hypothetical prote	1105	63.5	5.3	544	2	C96943	sterol O-acetyltrans
1033	63.5	5.3	231	2	F85679	probable antitrepre	1106	63.5	5.3	551	2	B64537	uncharacterized me
1034	63.5	5.3	238	2	F85336	hypothetical prote	1107	63.5	5.3	551	2	D71969	L-lactate permease
1035	63.5	5.3	241	2	F86691	ABC transporter pe	1108	63.5	5.3	555	2	G96744	probable peptidase
1036	63.5	5.3	242	1	S74794	branched-chain ami	1109	63.5	5.3	567	2	C75340	probable L-lactate
1037	63.5	5.3	246	2	AD3574	hypothetical prote	1110	63.5	5.3	568	2	T17588	hyaluronoglucosamyl
1038	63.5	5.3	259	2	AF0106	probable membrane	1111	63.5	5.3	593	2	I46528	sodium/dicarboxyla
1039	63.5	5.3	275	2	E95161	hypothetical prote	1112	63.5	5.3	594	2	B88956	protein ZK697.5 [i
1040	63.5	5.3	275	2	D98027	hypothetical prote	1113	63.5	5.3	605	2	A36361	glucose transport
1041	63.5	5.3	275	2	G84320	hypothetical prote	1114	63.5	5.3	605	2	H71562	probable flagellar
1042	63.5	5.3	276	2	E96951	conserved membrane	1115	63.5	5.3	605	2	T43974	hypothetical prote
1043	63.5	5.3	280	2	T16240	hypothetical prote	1116	63.5	5.3	610	2	T44161	hypothetical prote
1044	63.5	5.3	282	2	AB0346	probable ABC trans	1117	63.5	5.3	668	2	B54759	ba-type ubiquinol
1045	63.5	5.3	291	2	E83086	conserved hypotnet	1118	63.5	5.3	681	2	BF7237	protein kinase C (
1046	63.5	5.3	291	2	AB2939	hypothetical prote	1119	63.5	5.3	681	2	AF0697	probable type III
1047	63.5	5.3	291	2	E98343	hypothetical prote	1120	63.5	5.3	683	2	A85044	hypothetical prote
1048	63.5	5.3	291	2	F75571	hypothetical prote	1121	63.5	5.3	708	2	K01148	killer toxin KHS p
1049	63.5	5.3	313	2	D26696	NMDH2 dehydrogenas	1122	63.5	5.3	741	2	T20314	hypothetical prote
1050	63.5	5.3	315	2	B69365	hypothetical prote	1123	63.5	5.3	760	2	T48189	probable transport
1051	63.5	5.3	316	2	H86665	ferrichrome ABC tr	1124	63.5	5.3	787	2	A70132	cell division prot

1125	63.5	5.3	819	2	T19351	1198	63	5.3	480	2	B70367	hypothetical prote
1126	63.5	5.3	841	2	T38703	1199	63	5.3	481	2	S60260	stromatin-like prot
1127	63.5	5.3	843	2	T32487	1200	63	5.3	480	2	C71541	probable na-depend
1128	63.5	5.3	843	2	T41237	1201	63	5.3	491	2	AC1499	transmembrane prot
1129	63.5	5.3	843	2	AD2339	1202	63	5.3	493	2	T02376	hypothetical prote
1130	63.5	5.3	951	2	T08987	1203	63	5.3	494	2	T14246	NADH2 dehydrogenas
1131	63.5	5.3	966	2	H97717	1204	63	5.3	508	2	E90594	amino acid permeas
1132	63.5	5.3	1004	2	G87323	1205	63	5.3	509	1	A48528	membrane glycoprot
1133	63.5	5.3	1098	2	S38100	1206	63	5.3	527	2	T40744	probable nuclear d
1134	63.5	5.3	1229	2	S42381	1207	63	5.3	531	2	AH1491	hypothetical prote
1135	63.5	5.3	1351	2	C71607	1208	63	5.3	533	2	T06153	hypothetical prote
1136	63.5	5.3	1388	2	T11769	1209	63	5.3	534	2	A99316	hypothetical prote
1137	63.5	5.3	1407	1	T10558	1210	63	5.3	535	2	AF1835	hypothetical prote
1138	63.5	5.3	1408	2	T47671	1211	63	5.3	562	2	B70081	hypothetical prote
1139	63.5	5.3	1545	2	T42751	1212	63	5.3	565	2	B86359	protein similar to
1140	63.5	5.3	1545	2	T46645	1213	63	5.3	569	2	C70136	flagellar basal-bo
1141	63.5	5.3	1769	2	S53378	1214	63	5.3	574	2	T47566	hypothetical prote
1142	63.5	5.3	2357	2	A59249	1215	63	5.3	579	2	AB2177	hypothetical prote
1143	63.5	5.3	4725	1	A44357	1216	63	5.3	583	2	G84829	probable PIR2 faml
1144	63	5.3	96	1	MMVZP3	1217	63	5.3	584	2	G89789	two-component sens
1145	63	5.3	103	2	T20878	1218	63	5.3	598	2	S66954	probable membrane
1146	63	5.3	175	2	D70945	1219	63	5.3	600	2	B83875	two-component sens
1147	63	5.3	230	2	B81705	1220	63	5.3	608	2	AD2000	ABC transporter At
1148	63	5.3	230	2	T17506	1221	63	5.3	677	2	T26574	hypothetical prote
1149	63	5.3	236	2	F83520	1222	63	5.3	677	2	F95910	probable membrane-
1150	63	5.3	249	2	T01891	1223	63	5.3	682	1	H64485	replicational licens
1151	63	5.3	257	2	S01165	1224	63	5.3	701	2	T13568	NADH2 dehydrogenas
1152	63	5.3	258	2	H65188	1225	63	5.3	702	2	T12677	NADH2 dehydrogenas
1153	63	5.3	258	2	F86071	1226	63	5.3	704	2	T13665	NADH2 dehydrogenas
1154	63	5.3	258	2	H91224	1227	63	5.3	712	2	D87418	proton pump, proba
1155	63	5.3	280	2	D84015	1228	63	5.3	729	2	T06127	probable sugar tra
1156	63	5.3	288	2	S36954	1229	63	5.3	737	2	T39547	5-protein secretio
1157	63	5.3	290	2	S48301	1230	63	5.3	738	2	S58612	NADH2 dehydrogenas
1158	63	5.3	301	2	T50001	1231	63	5.3	769	2	G95270	hypothetical prote
1159	63	5.3	306	2	H83620	1232	63	5.3	813	2	T02672	hypothetical prote
1160	63	5.3	313	2	A86743	1233	63	5.3	849	2	C87740	protein H26D21.2 [
1161	63	5.3	322	2	B90013	1234	63	5.3	869	2	S49844	probable membrane
1162	63	5.3	332	2	B87790	1235	63	5.3	943	2	B45082	neurotrophic recep
1163	63	5.3	332	2	B84943	1236	63	5.3	960	2	T17297	hypothetical prote
1164	63	5.3	339	2	D89880	1237	63	5.3	1030	2	A42497	anion exchanger 3,
1165	63	5.3	345	2	T12364	1238	63	5.3	1034	2	B86880	SWI/SNF family hel
1166	63	5.3	358	2	B83808	1239	63	5.3	1082	2	H70360	cation efflux syst
1167	63	5.3	359	2	S56720	1240	63	5.3	1212	2	B82809	exodeoxyribonuclea
1168	63	5.3	361	2	A45211	1241	63	5.3	1227	2	B34911	band 3-related pro
1169	63	5.3	362	2	T29552	1242	63	5.3	1532	2	T18438	hypothetical prote
1170	63	5.3	362	2	C69804	1243	63	5.3	1646	2	JH0422	voltage-dependent
1171	63	5.3	364	2	S65009	1244	63	5.3	1854	2	T39035	putative sodium ch
1172	63	5.3	365	2	A42414	1245	63	5.3	2203	2	T42742	voltage-dependent
1173	63	5.3	378	1	S17412	1246	63	5.3	2295	2	B71621	probable membrane
1174	63	5.3	379	1	S17411	1247	63	5.3	4488	1	RR1M2	genome polypeptin
1175	63	5.3	379	1	S41833	1248	62.5	5.2	107	2	B69262	hypothetical prote
1176	63	5.3	379	1	S41847	1249	62.5	5.2	140	2	B86739	potassium channel
1177	63	5.3	379	1	S43265	1250	62.5	5.2	149	2	B83851	hypothetical prote
1178	63	5.3	379	1	T11492	1251	62.5	5.2	168	2	JC1169	DNA-damage-inducib
1179	63	5.3	379	2	S58085	1252	62.5	5.2	173	2	D71702	hypothetical prote
1180	63	5.3	379	2	S58464	1253	62.5	5.2	178	2	S67379	hypothetical prote
1181	63	5.3	382	2	S47882	1254	62.5	5.2	181	2	G82811	hypothetical prote
1182	63	5.3	386	2	S60646	1255	62.5	5.2	200	2	A71895	hypothetical prote
1183	63	5.3	389	2	H95003	1256	62.5	5.2	232	2	T22698	hypothetical prote
1184	63	5.3	389	2	C97876	1257	62.5	5.2	236	2	F83705	hypothetical prote
1185	63	5.3	391	2	D64541	1258	62.5	5.2	240	2	H70091	hypothetical prote
1186	63	5.3	396	2	E97947	1259	62.5	5.2	244	2	T20810	hypothetical prote
1187	63	5.3	398	2	E70415	1260	62.5	5.2	245	2	S10658	hypothetical prote
1188	63	5.3	405	2	T20902	1261	62.5	5.2	258	2	E91201	type III secretion
1189	63	5.3	411	2	G90154	1262	62.5	5.2	258	2	A86048	esct (imported) -
1190	63	5.3	415	2	S39535	1263	62.5	5.2	274	2	AC2946	hypothetical prote
1191	63	5.3	420	2	A57742	1264	62.5	5.2	274	2	G98336	sorbitol/mannitol
1192	63	5.3	431	2	T23809	1265	62.5	5.2	276	2	G72292	glycerol-3-phospha
1193	63	5.3	448	2	T30982	1266	62.5	5.2	276	2	H83568	probable permease
1194	63	5.3	450	2	A34169	1267	62.5	5.2	280	2	T24579	hypothetical prote
1195	63	5.3	469	2	A82188	1268	62.5	5.2	283	2	T11063	NADH2 dehydrogenas
1196	63	5.3	475	2	S52893	1269	62.5	5.2	289	2	D82504	phosphate ABC tran
1197	63	5.3	478	2	CS9095	1270	62.5	5.2	293	2	AH0075	probable permease

1271	62.5	5.2	296	2	H83460	cytochrome o ubiq	1344	62.5	5.2	704	2	S46000	probable membrane
1272	62.5	5.2	298	2	T37251	homeobox protein c	1345	62.5	5.2	718	2	T05840	subtilisin-like pr
1273	62.5	5.2	299	2	T26365	hypothetical prote	1346	62.5	5.2	732	2	T27937	hypothetical prote
1274	62.5	5.2	326	2	G90272	hypothetical prote	1347	62.5	5.2	807	2	T28379	ORF MSVII9 probabl
1275	62.5	5.2	333	2	AB1925	hypothetical prote	1348	62.5	5.2	815	2	G97266	mannose-1-phosphat
1276	62.5	5.2	333	2	B89010	hypothetical prote	1349	62.5	5.2	837	2	D71027	hypothetical prote
1277	62.5	5.2	335	2	T41426	hypothetical wt8	1350	62.5	5.2	848	2	A33810	band 3 anion trans
1278	62.5	5.2	349	2	H95060	ABC transporter, p	1351	62.5	5.2	865	2	AB1658	probable membrane
1279	62.5	5.2	349	2	D97929	hypothetical prote	1352	62.5	5.2	881	2	G96574	hypothetical prote
1280	62.5	5.2	352	2	B81450	probable integral	1353	62.5	5.2	971	2	H71719	hypothetical prote
1281	62.5	5.2	358	2	B83829	hypothetical prote	1354	62.5	5.2	1082	2	T41988	hypothetical prote
1282	62.5	5.2	365	2	B82210	amino acid ABC tra	1355	62.5	5.2	1144	2	A81983	probable DNA-dirc
1283	62.5	5.2	369	2	C88030	protein F46F5.10 f	1356	62.5	5.2	1195	2	C87691	hypothetical prote
1284	62.5	5.2	370	2	C69309	conserved hypochet	1357	62.5	5.2	1291	2	T17242	hypothetical prote
1285	62.5	5.2	379	1	S17407	ubiquinol-cytochro	1358	62.5	5.2	1391	2	T20642	hypothetical prote
1286	62.5	5.2	379	2	S58462	ubiquinol-cytochro	1359	62.5	5.2	1397	2	B87998	protein F09C3.1 f1
1287	62.5	5.2	379	2	S58057	ubiquinol-cytochro	1360	62.5	5.2	1576	2	T21172	hypothetical prote
1288	62.5	5.2	382	2	A72373	conserved hypochet	1361	62.5	5.2	1676	2	E71410	probable centromer
1289	62.5	5.2	383	1	A44227	omega-3 fatty acid	1362	62.5	5.2	1687	2	T43144	vitellogenin II pr
1290	62.5	5.2	383	2	F84771	hypothetical prote	1363	62.5	5.2	1951	2	B43963	RNA viral polymera
1291	62.5	5.2	383	2	T31738	hypothetical prote	1364	62.5	5.2	2150	2	S13553	hypothetical prote
1292	62.5	5.2	388	2	C64722	Na+/H+-exchanging	1365	62.5	5.2	11073	2	D82954	NADH2 dehydrogenas
1293	62.5	5.2	391	2	A86632	aromatic amino aci	1366	62.5	5.2	132	2	D82954	hypothetical prote
1294	62.5	5.2	399	2	H84087	hypothetical prote	1367	62.5	5.2	174	2	B84028	cell-shape determi
1295	62.5	5.2	404	2	H83249	sodium/glutamate s	1368	62.5	5.2	175	1	IMECB	colicin B immunity
1296	62.5	5.2	405	1	Q08B35	BRF3 protein - hu	1369	62.5	5.2	198	2	E97217	uncharacterized co
1297	62.5	5.2	406	2	H89006	protein T22F3.11 f	1370	62.5	5.2	201	2	G90134	hypothetical prote
1298	62.5	5.2	409	2	C89942	conserved hypochet	1371	62.5	5.2	206	2	F89840	conserved hypochet
1299	62.5	5.2	413	2	AC1369	multidrug resistanc	1372	62.5	5.2	209	2	A88656	protein F37C4.1 f4
1300	62.5	5.2	417	2	T51457	glucose 6 phosphat	1373	62.5	5.2	209	2	T32573	hypothetical prote
1301	62.5	5.2	420	2	D95018	conserved hypochet	1374	62.5	5.2	225	2	B65127	type 4 prepillin-11
1302	62.5	5.2	420	2	B97891	conserved hypochet	1375	62.5	5.2	242	1	F75433	probable phosphos
1303	62.5	5.2	422	2	C70518	probable nanp prot	1376	62.5	5.2	247	2	AC1332	potassium channel
1304	62.5	5.2	425	2	B97172	flagellin f1mporte	1377	62.5	5.2	273	2	E70010	dihydrolipoamide S
1305	62.5	5.2	426	2	A72080	CT266 hypothetical	1378	62.5	5.2	285	2	H95943	probable sugar upt
1306	62.5	5.2	426	2	B86542	hypothetical prote	1379	62.5	5.2	287	2	A69838	transcription regu
1307	62.5	5.2	431	2	H84069	hypothetical prote	1380	62.5	5.2	288	2	S36953	cytochrome-c oxida
1308	62.5	5.2	440	2	T20092	hypothetical prote	1381	62.5	5.2	288	2	C83356	probable permease
1309	62.5	5.2	442	1	J01042	endothelin recepto	1382	62.5	5.2	298	2	T29189	hypothetical prote
1310	62.5	5.2	443	2	F30010	NADH2 dehydrogenas	1383	62.5	5.2	305	2	T43972	hypothetical prote
1311	62.5	5.2	443	2	T08136	probable omega-6 d	1384	62.5	5.2	306	2	A10209	probable sugar ABC
1312	62.5	5.2	452	2	G85647	hypothetical prote	1385	62.5	5.2	306	2	T41290	conserved hypochet
1313	62.5	5.2	452	2	G90787	hypothetical prote	1386	62.5	5.2	312	2	S48851	chalcone reductase
1314	62.5	5.2	452	2	G64844	probable membrane	1387	62.5	5.2	312	2	S48849	hypothetical prote
1315	62.5	5.2	455	2	D97217	glycosyltransferas	1388	62.5	5.2	315	2	T24821	hypothetical prote
1316	62.5	5.2	457	2	F69662	UDP-N-acetylmuramo	1389	62.5	5.2	331	2	AB3117	hypothetical prote
1317	62.5	5.2	459	2	AP3284	high-affinity bran	1390	62.5	5.2	344	2	T05987	hypothetical prote
1318	62.5	5.2	461	2	S57713	probable mannosyl	1391	62.5	5.2	345	2	T32203	hypothetical prote
1319	62.5	5.2	468	2	A49131	inositol 1,4,5-tri	1392	62.5	5.2	351	2	C86408	F3H9.12 protein -
1320	62.5	5.2	470	2	C70641	hypothetical prote	1393	62.5	5.2	352	2	C98170	hypothetical prote
1321	62.5	5.2	487	2	S73161	hypothetical prote	1394	62.5	5.2	353	2	T42971	hypothetical prote
1322	62.5	5.2	490	2	T40116	hypothetical prote	1395	62.5	5.2	360	2	A53611	interleukin-8 rece
1323	62.5	5.2	492	2	AC0768	probable transmemb	1396	62.5	5.2	360	2	T33260	hypothetical prote
1324	62.5	5.2	494	1	T15502	hypothetical prote	1397	62.5	5.2	362	2	B57641	G protein-coupled
1325	62.5	5.2	501	2	JN0539	head protein sps -	1398	62.5	5.2	363	2	S42379	hypothetical prote
1326	62.5	5.2	502	2	C86263	hypothetical prote	1399	62.5	5.2	370	2	H84111	response regulator
1327	62.5	5.2	505	2	S44647	f42h10.1 protein -	1400	62.5	5.2	377	2	T05427	hypothetical prote
1328	62.5	5.2	507	2	S52677	probable membrane	1401	62.5	5.2	379	2	S58457	ubiquinol-cytochro
1329	62.5	5.2	546	2	AB0571	probable membrane	1402	62.5	5.2	379	2	B58851	ubiquinol-cytochro
1330	62.5	5.2	547	2	S64332	probable membrane	1403	62.5	5.2	381	2	T11440	probable two-compo
1331	62.5	5.2	568	2	S64567	probable membrane	1404	62.5	5.2	383	2	C95965	bicyclomyacin resis
1332	62.5	5.2	569	2	T12928	hypothetical prote	1405	62.5	5.2	398	1	B64112	hypothetical prote
1333	62.5	5.2	572	2	T11478	NADH2 dehydrogenas	1406	62.5	5.2	399	2	F72417	translocation prot
1334	62.5	5.2	578	2	I56215	interleukin-10 rec	1407	62.5	5.2	399	2	JC5279	cell-division prot
1335	62.5	5.2	580	2	T02596	hypothetical prote	1408	62.5	5.2	400	2	AB1565	xylose operon regu
1336	62.5	5.2	601	2	T11451	NADH2 dehydrogenas	1409	62.5	5.2	402	2	D70186	conserved hypochet
1337	62.5	5.2	608	2	T34381	hypothetical prote	1410	62.5	5.2	403	2	B69338	cbs domain protein
1338	62.5	5.2	610	2	A28798	myosin-light-chain	1411	62.5	5.2	411	2	H72084	protein-tyrosine-p
1339	62.5	5.2	621	2	B95897	probable cellulose	1412	62.5	5.2	432	1	A34845	hypothetical prote
1340	62.5	5.2	638	2	G02068	white homolog - hu	1413	62.5	5.2	432	2	T21880	hypothetical prote
1341	62.5	5.2	668	2	T1868	hypothetical prote	1414	62.5	5.2	444	2	T47737	probable transmemb
1342	62.5	5.2	668	2	T04073	intensifier 1 prot	1415	62.5	5.2	444	2	F81367	hypothetical prote
1343	62.5	5.2	697	2	T19254	hypothetical prote	1416	62.5	5.2	454	2	H65054	hypothetical prote

1417	62	5.2	458	2	A84487
1418	62	5.2	466	2	AH1800
1419	62	5.2	474	2	E64232
1420	62	5.2	483	2	E46124
1421	62	5.2	487	2	T05271
1422	62	5.2	497	1	S53834
1423	62	5.2	497	2	666834
1424	62	5.2	499	2	B81914
1425	62	5.2	502	2	AE2372
1426	62	5.2	514	2	A96671
1427	62	5.2	528	1	ACCH2N
1428	62	5.2	555	2	T08869
1429	62	5.2	567	2	S29498
1430	62	5.2	582	2	S19424
1431	62	5.2	585	2	T02360
1432	62	5.2	600	2	AD3138
1433	62	5.2	600	2	H98149
1434	62	5.2	630	2	H83686
1435	62	5.2	644	2	T20034
1436	62	5.2	660	2	A44432
1437	62	5.2	667	2	T20739
1438	62	5.2	675	1	S46952
1439	62	5.2	675	2	T20822
1440	62	5.2	678	2	F71921
1441	62	5.2	702	2	T03903
1442	62	5.2	707	2	A35804
1443	62	5.2	724	1	HMS884
1444	62	5.2	739	2	T25030
1445	62	5.2	743	2	A29232
1446	62	5.2	750	2	S73829
1447	62	5.2	756	2	A88679
1448	62	5.2	791	2	A46616
1449	62	5.2	810	1	A33380
1450	62	5.2	841	2	T09455
1451	62	5.2	848	2	E95092
1452	62	5.2	864	2	T42556
1453	62	5.2	872	1	TNBBEH
1454	62	5.2	911	2	S70958
1455	62	5.2	932	2	C70131
1456	62	5.2	950	1	FMBYR1
1457	62	5.2	1002	2	A97217
1458	62	5.2	1024	2	AE3557
1459	62	5.2	1030	2	T13163
1460	62	5.2	1031	2	T43458
1461	62	5.2	1041	2	T29010
1462	62	5.2	1242	2	G88480
1463	62	5.2	1273	2	C96767
1464	62	5.2	1283	2	T18939
1465	62	5.2	1321	2	A60165
1466	62	5.2	1780	2	T20695
1467	62	5.2	1802	2	T33783
1468	62	5.2	6359	2	T31679
1469	61.5	5.1	99	2	B99233
1470	61.5	5.1	134	2	B69985
1471	61.5	5.1	149	2	C86655
1472	61.5	5.1	150	2	S43955
1473	61.5	5.1	159	2	S77185
1474	61.5	5.1	162	2	AF2618
1475	61.5	5.1	162	2	B97400
1476	61.5	5.1	163	2	JC5045
1477	61.5	5.1	173	2	H97775
1478	61.5	5.1	176	2	G89947
1479	61.5	5.1	176	2	S40726
1480	61.5	5.1	183	2	H70478
1481	61.5	5.1	185	2	H69337
1482	61.5	5.1	190	2	A26630
1483	61.5	5.1	212	2	A83521
1484	61.5	5.1	225	2	T19811
1485	61.5	5.1	264	2	T18998
1486	61.5	5.1	272	2	G82888
1487	61.5	5.1	273	2	T28980
1488	61.5	5.1	274	2	S42168
1489	61.5	5.1	276	2	F72342

probable replicati
transmembrane effl
hypothetical prote
nuclear protein EN
probable 3-oxoacyl
NMDH2 dehydrogenas
probable membrane
probable periplasm
hypothetical prote
Ammonium transport
nucleoside acetylch
protein P2 - Acyryl
lymphocyte antigen
hypothetical prote
hypothetical prote
ATP-binding transp
PTS system, beta-g
hypothetical prote
amino acid transpo
hypothetical prote
phosphotransferase
hypothetical prote
hypothetical prote
nucleolin - human
heat shock protein
hypothetical prote
101k malaria antiq
probable ABC trans
protein H06H21.10
cytochrome-c oxide
interleukin-4 rece
vacuolar assembly
antipeptidase N
regument protein 1
97K alpha trans-in
cena protein - Vib
penicillin-binding
Ca2+-transporting
conserved membrane
acetylflavin resista
Rab6 GTPase activa
hypothetical prote
hypothetical prote
protein C16a3.7
unknown protein F2
hypothetical prote
sodium channel pro
hypothetical prote
bacteracl synthe
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
probable NMDH2 deh
hypothetical prote
lipoprotein signal
hypothetical prote
epithelial membran
hypothetical prote
hypothetical prote
hypothetical prote
hypothetical prote
conserved hypochet
nucleoplasm A -
conserved hypochet
hypothetical prote
hypothetical prote
hypothetical prote
NMDH2 dehydrogenas
conserved hypochet

1490	61.5	5.1	278	2	D83080
1491	61.5	5.1	279	2	AG0421
1492	61.5	5.1	284	2	AC3429
1493	61.5	5.1	289	2	F91269
1494	61.5	5.1	289	2	D86110
1495	61.5	5.1	290	2	AE0947
1496	61.5	5.1	292	2	AE1539
1497	61.5	5.1	293	2	C90032
1498	61.5	5.1	293	2	A83710
1499	61.5	5.1	293	2	B69866
1500	61.5	5.1	294	2	AD0886

ALIGNMENTS

RESULT 1
138027
MLN 64 protein - human
C/Species: Homo sapiens (man)
C/Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C/Accession: I38027; S60682
R/Tomasetto, C.; Regnier, C.H.; Moog-Lutz, C.; Mattei, M.G.; Chénard, M.P.; Lidereau, R.,
Genomics 28, 367-376, 1995
A/Title: Identification of four novel human genes amplified and overexpressed in breast c
A/Reference number: I37080; MUID:96039245; PMID:7490069
A/Accession: I38027
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: mRNA
A/Residues: 1-445 <RES>
A/Cross-references: UNIPROT:Q14849; EMBL:X80196; NID:951278; PIDN:CA56489.1; PID:95127;
C/Note: submitted to the EMBL Data Library, July 1994
C/Genetic:
A/Gene: MLN64

Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 1.2e-54;
Matches 135; Conservative 38; Mismatches 45; Indels 22; Gaps 5;

QY 1 MNDP-----EDMENL-----TGSQSHASLRNHSINPQLMARISYGRKKIGSDV 51
DB 1 MSKLPRELTDLRSLPAVASLSGSSLSHSQSLSLPPE-----KRRALSDV 49
QY 52 RRRFCLFVTFEDLLFVTLMTIILNVNGIENTLEKVMQDYSSYDFILAVFRKVL 111
DB 50 RRRFCLFVTFEDLLFVTLMTIILNVNGIENTLEKVMQDYSSYDFILAVFRKVL 109
QY 112 ILAVAVCRRLHMMVAALITVAVTSAPFLAKVILSKLFSQGAFGVLPPIISFLAMIEITWFL 171
DB 110 LIGYAVLQRLHMMVAVITVTSAPFLAKVILSKLFSQGAFGVLPPIISFLAMIEITWFL 169
QY 172 DFRVLPQAEERERLLIVDASERRAII-EGSLSDGQFYSPPSSEAGSE-BAEERKQDSEK 229
DB 170 DFRVLPQAEERERWYLAQVAVARGPLIFSGALSGCFYSPPSFAGSDNESDEEVAGKK 229

RESULT 2
T16170
hypothetical protein F26F4.4 - Caenorhabditis elegans
C/Species: Caenorhabditis elegans
C/Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C/Accession: T16170
R/Fulton, U.
submitted to the EMBL Data Library, March 1996
A/Description: The sequence of C. elegans cosmid F26F4.
A/Reference number: Z18471
A/Accession: T16170
A/Status: preliminary; translated from GB/EMBL/DBJ
A/Molecule type: DNA
A/Residues: 1-478 <FUL>
A/Cross-references: UNIPROT:Q19819; EMBL:U12964; NID:91233452; PID:9529202; PIDN:AAA9121;
A/Experimental source: strain Bristol N2
C/Genetic:

A:Gene: CESP.F26P4.4
A:Introns: 47/2; 81/2; 125/3; 171/3; 214/1; 236/2; 343/3; 444/1
Query Match 17.1%; Score 204; DB 2; Length 478;
Best Local Similarity 26.5%; Pred. No. 2.7e-11;
Matches 56; Conservative 36; Mismatches 73; Indels 46; Gaps 6;
QY 42 GREKKGSDVRRRTCLFVTDLFVTLMLT-----ELNVNGIENTLEK 86
DB 69 GSGRGVSKRKRIIVTFPDTSTIILMLCTYTRDDMDKVFENEINT-----FNP 121
QY 87 EVMQDYSSYFDIFLLAVPRFKVLILAVACRLRHMAIALTTAVTSAILAVILSKL 146
DB 122 KFIIRI-----SLFDIVILAVRMLILGVYGCIVKQWTVAVFTLASSAYILMKVLFYFN 177
QY 147 FSGCAFQVLPITL-SFLIWIETWFLDKVLPOEAEEENLLIYQDASERAAALPGSLD 205
DB 178 HSSSAVPLLLITLTSFTLCSEFYLMPPQILPRERYARRRL-----DGIEN 224
QY 206 GQFYSPESEA-----GSEAEKQDESKP 230
DB 225 PEFETDDEARSNNRRGRQONGSGNSEAP 255

RESULT 3

H90281
hypothetical protein dppB-1 (imported) - Sulfolobus solfataricus
C:Species: Sulfolobus solfataricus
C>Date: 24-May-2001 #sequence_revision 24-May-2001 #text_change 09-Jul-2004
C/Accession: H90281
R:She, Q.; Singh, R.K.; Confalonieri, F.; Zivanovic, Y.; Allard, G.; Awayez, M.J.; Chan-
Jong, I.; Jeffries, A.C.; Kozera, C.J.; Medina, N.; Peng, X.; Thi-Ngoc, H.P.; Redder, F.
arlett, R.A.; Ragan, M.A.; Senen, C.W.; Van der Oost, J.
submitted to GenBank, April 2001
A:Description: Sulfolobus solfataricus complete genome.
A:Reference number: A99139
A:Accession: H90281
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-348 <KIR>
A:Cross-references: UNIPROT:Q9Y7Q0; GB:AB006641; NID:g13814471; PIDN:AAK41511.1; GSPDB:C
A:Genetics:
A:Gene: dppB-1
Query Match 8.6%; Score 102.5; DB 2; Length 348;
Best Local Similarity 23.7%; Pred. No. 0.066;
Matches 49; Conservative 35; Mismatches 66; Indels 57; Gaps 9;
QY 15 SQSSHASLRNHSINPTQLMARISYGREKKGISDVRRTCLFVTDLFVTLMLTEL 74
DB 46 AQFSQTLFKNAHNLNSTQIQLAVEKY--RE-----SLIAAYGL 81
QY 75 NVNNGIENTLEK-----EVMQDYSSYFDIFLLAVPRFKVLILAVACRLRHMAIAL 128
DB 82 N-----OPTIDKVFIQWNLNMFDFGTAYF-LQAPSSGREVSSILAYLPLN-----TTL 130
QY 129 TTAVTSAILAVILSKLFGSGAF-GVYLPIISFLIWIETWFLDKVLPOEAEEENLL 187
DB 131 FTTRATVFIYAGTIIIGLSAKSKMEKVIATIIAIVHSIPTWLG-----VL 178
QY 188 IVODASERAAALPGSLDQGFYSPES 214
DB 179 IAAALAVAVKVPFGWMTS---VPEPKN 202
RESULT 4
D75080
glucose-1-phosphate thymidyltransferase related protein PAB2433 - Pyrococcus abyssi (S
C:Species: Pyrococcus abyssi
C>Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 09-Jul-2004
C/Accession: D75080
R:anonymous, Genoscope
submitted to the EMBL Data Library, July 1999

A:Description: Pyrococcus abyssi genome sequence: insights into archaeal chromosome struc
A:Reference number: A75001
A:Accession: D75080
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-424 <KAW>
A:Cross-references: UNIPROT:Q9UZW1; GB:AJ248286; GB:AL096836; NID:g5458366; PIDN:CAB4994;
A:Experimental source: strain Orsay
C:Genetics:
A:Gene: PAB2433
C:Superfamily: Aquifex aeolicus glucose-1-phosphate thymidyltransferase

Query Match 7.8%; Score 93.5; DB 2; Length 424;
Best Local Similarity 21.9%; Pred. No. 0.59;
Matches 47; Conservative 25; Mismatches 72; Indels 71; Gaps 7;

QY 5 PEDMEN-----LNGSSHASLRNHSINPTQLMARISYSGRE 44
DB 207 PEDIKKARKLIIVTSYKVGDFISRLNRKISTRSLALVEHVTPQM----- 255
QY 45 KKGISDVRRTCLFVTDL-LFVTLMLTIELNVNG-----GIENLEKVMQDY 93
DB 256 -----TIVTFPGIFGALNFIISVPIAGIIVYSSILDGVDGSIARARQTSK 303
QY 94 YSSYFDIFLLAVPRFK-VLILAVACRLRHMAIALTTAVTSAIL-----L 138
DB 304 FGCGFDSILDRVYDFELLILAVYSIREPLMMAIALMPSAMVSYSTERFGAYCVA 363
QY 139 AKYI--LSKLFSGARQVLPPIISFLIWIETWFL 171
DB 364 YKVIPLARKVPGKRDRIFFTLMLTIVGWIKALFL 398

RESULT 5

T43048
calcium channel alpha-1 chain - Cyanea capillata
C:Species: Cyanea capillata
C>Date: 11-Jan-2000 #sequence_revision 11-Jan-2000 #text_change 09-Jul-2004
C/Accession: T43048
R:Jezioriski, M.C.; Greenberg, R.M.; Clark, K.S.; Anderson, P.A.V.
J:Title: Cloning and functional expression of a voltage-gated calcium channel subu
A:Title: Cloning and functional expression of a voltage-gated calcium channel subu
A:Reference number: 222300; WUID:98380510; PMID:9712913
A:Accession: T43048
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-1911 <JEZ>
A:Cross-references: UNIPROT:O02038; EMBL:U03075; NID:g1947095; PID:g1947096; PIDN:AA630;
C:Superfamily: voltage-dependent calcium channel protein alpha-1 chain
C:Keywords: transmembrane protein

Query Match 7.5%; Score 90; DB 2; Length 1911;
Best Local Similarity 23.5%; Pred. No. 7.3;
Matches 43; Conservative 33; Mismatches 59; Indels 48; Gaps 9;

QY 5 PEDMENALNGSSHASLRNHSINPTQLM-----ARISYEGREKKGISDV----- 51
DB 791 PEDVE--LGNPKSKNGTLRMGTTSTEMSGEAKRIRPLRLSLMLDKOIPMPMPRESS 848
QY 52 -----RRTCLFVTPLLVTL-LMLTIELNVNGIENTLEKVMQDYSSYFDI 100
DB 849 FFIISANNKRLRYLCYRLAVNKKIFINSLIVLIISSVALAEDPIGRDVLR-NKILGFDI 907
QY 101 FLIIVPRFKVLI--LAVAV-----CR-----LRHMAIALTT-AVTSAILA 139
DB 908 FTTRATVFIYAGTIIIGLSAKSKMEKVIATIIAIVHSIPTWLG-----VL 178
QY 140 KVI 142
DB 968 RVL 970

RESULT 6

QY 98 FDIPLAVFRKVLILAVACRLRHWMAIALTTAVTSAPLAKVY--LSKLFSGA----- 151
 Db 331 LITSVLPIFSFPAYIYTL-KYSHLIGILIRSVSAFPAALAFQVLFGFRGASPSF 389
 QY 152 -----FGYVLPITISFILAMIEFWLDFKVLPOEAEENRLLIV-----QDASRAA 197
 Db 390 GAIMEGSVTFEYVYIP-LAFVLA-----NTYNNLPFE-----ILVFIPELBDAILKLV 434
 QY 198 LIPGSLDQGFYS 210
 Db 435 SLP-----YFYS 441

RESULT 10

A41680
 integral membrane protein ppsa - Chinese hamster
 C:Species: Crictetus griseus (Chinese hamster)
 C>Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 06-Oct-2000
 C:Accession: A41680
 R:Kuge, O.; Nishijima, M.; Akamatsu, Y.
 J. Biol. Chem. 266, 24184-24189, 1991
 A:Title: A Chinese hamster CDNA encoding a protein essential for phosphatidylserine synthase
 A:Reference number: A41680; MUID:92084723; PMID:1748687
 A:Accession: A41680
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-471 <KUR>
 A:Cross-references: GB:D90468; NID:g220280; PIDN:BA01084.1; PID:dl001553; PI
 C:Superfamily: Caenothabditis elegans hypothetical protein ZC506.3
 C:Keywords: membrane protein

Query Match 7.1%; Score 84.5; DB 2; Length 471;
 Best Local Similarity 24.4%; Pred. No. 4.7;
 Matches 32; Conservative 22; Mismatches 38; Indels 39; Gaps 7;
 QY 55 FCLFVFDLLFVTLMTIELNVNGIENLEKEVMQY-----DYSSYDFDILAV 105
 Db 117 FLPLNFEQVSLMYW-LDPLRYA---TREADIMEYAVNCHVITWRIVSHDFIFAFGH 172
 QY 106 F----RRKVLILAVACRLRHWMAIALTTAVTSAPLAKVYLSLFGQAFGYVLPITISF 161
 Db 173 FVGWAKALILIRSYGLC---WTISITWELTELF-----FMHLLP--NF 210
 QY 162 ILAWIETWFLD 172
 Db 211 AECWMDVILD 221

RESULT 11

H97002
 probable integral membrane protein [imported] - Clostridium acetobutylicum
 C:Species: Clostridium acetobutylicum
 C>Date: 14-Sep-2001 #sequence_revision 14-Sep-2001 #text_change 09-Jul-2004
 C:Accession: H97002
 R:Moiling, J.; Breton, G.; Ometchenko, M.V.; Markarova, K.S.; Zeng, Q.; Gibson, R.; Lee, J.; Daly, M.J.; Bennett, G.N.; Koonin, E.V.; Smith, D.R.
 J. Bacteriol. 183, 4823-4838, 2001
 A:Title: Genome Sequence and Comparative Analysis of the Solvent-Producing Bacterium Cld
 A:Reference number: A96900; MUID:21359325; PMID:21359325
 A:Accession: H97002
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-352 <KUR>
 A:Cross-references: UNIPROT:Q97KT1; GB:A8001437; PIDN:AAK7881.1; PID:g15023727; GSPDB:G
 A:Experimental source: Clostridium acetobutylicum ATCC824
 C:Genetics:
 A:Gene: CAC0835

Query Match 7.0%; Score 83.5; DB 2; Length 352;
 Best Local Similarity 19.2%; Pred. No. 4.1;
 Matches 38; Conservative 35; Mismatches 50; Indels 75; Gaps 8;

QY 38 ESEYERREKGISDVRRTFCLFVTD-----LIETLMTIEL 74
 Db 115 EFYNVDRDKTNEMDKLIKAYLVONKTNMERIVKDEQIGLSKSRRIIAFLATVLLITS 174
 QY 75 NNNGI-----ENTLEKEVMQ-----YDYSSYDFD-----LAVFRKVL 111
 Db 175 VVNGAVIIRDRRENTYRYWYSPNSKREYIEGNVITNYIPSYQLPLANSMLMIFGIYIG 234
 QY 112 I-----LAVACRLRHWMAIALTTAVTSAP-----LAKVILSKLFSGAFGYVLPITIS 160
 Db 235 ISFLKMLSYGL-----ILTVMTITGRTIVCIENKELVANNFSAA-----IS 276
 QY 161 FILAMIEFWLDFKVLPOQ 178
 Db 277 LILSVGTRINXKIMPE 294

RESULT 12

AE0302
 sugar ABC transporter, permease protein YPO2476 [imported] - Yersinia pestis (strain CO9;
 C:Species: Yersinia pestis
 C>Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
 C:Accession: AE0302
 R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.;
 deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; E
 11, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrett, T
 Nature 413, 523-527, 2001
 A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.
 A:Reference number: AB0001; MUID:21470413; PMID:11586560
 A:Accession: AE0302
 A:Status: preliminary
 A:Molecule type: DNA
 A:Residues: 1-291 <KUR>
 A:Cross-references: UNIPROT:Q8ZDT0; GB:AL590842; PIDN:CA691281.1; PID:g15980470; GSPDB:G
 C:Superfamily: inner membrane protein ugpa
 C:Gene: YPO2476

Query Match 6.9%; Score 83; DB 2; Length 291;
 Best Local Similarity 22.3%; Pred. No. 3.7;
 Matches 44; Conservative 26; Mismatches 57; Indels 70; Gaps 10;
 QY 46 KGISDVRRTFCLFVTDLLFVTLMTIELNVN-----GGINTL----- 84
 Db 9 KQVGSVLAASVGLGYSIFWFYFPIMLAVLSLTEMRFVGIPTEGNLNFILVMQDPLFWKS 68
 QY 85 EKEVMQDYSSYDFDILAVFRKVLILAVACRLRHWMAIALTTAVTSAPLAKVY--- 141
 Db 69 MLNVMRPLMY--VLPVFISSFLP-----AFGLQKLKHG---RTFVALSFLANVSSG 116
 QY 142 -----ILSKLFSGA-----FGYVLPITIS-----FILAMIEFW-----FL 171
 Db 117 VASIVPSKIFSGONGLNFILYMRFGFTLPWLTPSPFAMLSIALVYTWKFGVGYGLHS 176

QY 172 DFVFLPOE-----AEEN 184
 Db 177 GLNSIRPEIYSABELDN 193

RESULT 13

S34960
 NADH2 dehydrogenase (ubiquinone) (EC 1.6.5.3) chain 5 - Crithidia oncopelti mitochondrion
 C:Species: mitochondrion Crithidia oncopelti
 C>Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004
 C:Accession: S34960
 R:Kaeliov, D.A.; Horvath, A.; Gwang II, K.; Kolesnikov, A.A.
 submitted to the EMBL Data Library, October 1990
 A:Reference number: S34958
 A:Accession: S34960
 A:Molecule type: DNA
 A:Residues: 1-590 <NAS>
 A:Cross-references: UNIPROT:Q34192; EMBL:X56015; NID:g12879; PIDN:CA39492.1; PID:g12882

Query Match 7.0%; Score 83.5; DB 2; Length 352;
 Best Local Similarity 19.2%; Pred. No. 4.1;
 Matches 38; Conservative 35; Mismatches 50; Indels 75; Gaps 8;

A:Gene: ND5
A:genome: mitochondrion
A:genetic code: GCG
C:Superfamily: NADH dehydrogenase (ubiquinone) chain 5
C:Keywords: membrane-associated complex; mitochondrion; NAD; oxidative phosphorylation;

Query Match 6.9%; Score 83; DB 1; Length 590;

Best Local Similarity 23.9%; Pred. No. 8.4; Mismatches 37; Indels 42; Gaps 7;

Matches 32; Conservative 23; Mismatches 37; Indels 42; Gaps 7;

QY 55 FCLFVTP-----DLT-----FTLMTIELNVNGIENTLEKEVMQDYSSYFDIFLLAVF 106

DB 95 FILFVAFYVYVYDLMKRFNIFVWVFLCNVFI-----LSYDYLTAVCGWELGLF 146

QY 107 RFVLLIAYVCRHRHMAALTATVTSAPLAKVILSKLFSQAGFVYPIISFILAWI 166

DB 147 SF--FLISY-----FWYREFALKFQKSPFISKI-----GDVILLISFVMTFI 187

QY 167 ET-----WFLDE 173

DB 188 STGYGMNIFYVNF 201

RESULT 14

B29835

Tras protein - Escherichia coli plasmid pED208

C/Species: Escherichia coli

C/Date: 04-Aug-1988 #sequence_revision 04-Aug-1988 #text_change 09-Jul-2004

C/Accession: B29835

R/Finlay, B.B.; Paranchych, W.

J. Bacteriol. 166, 713-721, 1986

A>Title: Nucleotide sequence of the surface exclusion genes tras and trar from the IncF-

A/Reference number: A29835; MUID:86223783; PMID:3011738

A/Accession: B29835

A/Status: preliminary

A/Molecule type: DNA

A/Residues: 1-186 <FIN>

A/Cross-references: UNIPROT:P14498

A/Genetic:

A/Genome: plasmid

Query Match 6.9%; Score 82.5; DB 2; Length 186;

Best Local Similarity 23.8%; Pred. No. 2.4; Mismatches 40; Indels 35; Gaps 6;

Matches 31; Conservative 24; Mismatches 40; Indels 35; Gaps 6;

QY 61 FDLFTVLLMIIELVNGIENTLEKEVMQDYSSYFDIFLL-----AVFRKVLILAY 115

DB 44 FOLLFI-----IPDIFINSNR-----DYH--YFDTFVITLGSNAFFSLVFLMSTY 87

QY 116 AVCRRLRHMMAALTATVTSAPLAKVILSKLFSQAGFVYLPFI-----SFLAW 165

DB 88 NLVSLK-----ISLGSRTESVLLKLVKINSYGFLLMVNNAIVGCVLLSGGRFVAGL 143

QY 166 IETWFLDPKV 175

DB 144 GPSWFTYILI 153

RESULT 15

C64227

hypothetical protein homolog MG247 - Mycoplasma genitalium

C/Species: Mycoplasma genitalium

C/Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004

C/Accession: C64227

M./Fraser, C.M.; Gocayne, J.D.; White, O.; Adams, M.D.; Clayton, R.A.; Fleischmann, R.D.;

M./Fuhrmann, J.; Nguyen, D.; Uterback, T.R.; Saudek, D.M.; Phillips, C.A.; Merrick, J.

; C.A.; Venter, J.C.

Science 270, 397-403, 1995

A>Title: The minimal gene complement of Mycoplasma genitalium.

A/Reference number: A64200; MUID:96026346; PMID:7569993

A/Accession: C64227

A/Status: preliminary; nucleic acid sequence not shown; translation not shown

A/Residues: 1-239 <TIGR>
A/Cross-references: UNIPROT:P47489; GB:U39703; GB:I43967; NID:G3844835; PIDN:AACT1467.1;
A/Experimental source: strain G-37
A/Genetic code: GCG
C:Superfamily: Escherichia coli ygiH protein

Query Match 6.9%; Score 82.5; DB 1; Length 239;

Best Local Similarity 21.7%; Pred. No. 3.3; Mismatches 54; Indels 39; Gaps 8;

Matches 33; Conservative 26; Mismatches 54; Indels 39; Gaps 8;

QY 42 GREKGISDVRRITF-----CLFVFDLLFVTL--WIELNVNGIENTLEKEVMQYD 92

DB 42 GSKNPQATMSMRVFGKIGFLVAIFDAFGFAFLTLTIL---FRGLQGYLTKKYQST 98

QY 93 YSSYFDIFLLAV-----FRK---VILLAVNCRHRHMAI-----ALTAVTSA 135

DB 99 YFLSYLSCFPAATGHIIFPLVFKFKGKAATGGSLSAISLWMLICLAIWITLITKY 158

QY 136 FLAKVILSKLFSQAGFVYPIISFILAWI 167

DB 159 VSLASLITP-----FVLAVI--ILIRWLD 180

Search completed: May 17, 2005, 10:23:07
Job time : 35 secs

BEST AVAILABLE COPY

GenCore version 5.1.6
 OM protein - protein search, using sw model
 Run on: May 17, 2005, 10:19:51 ; Search time 75 Seconds
 (without alignments)
 1206.692 Million cell updates/sec

Title: US-10-063-518-14
 Perfect score: 1195
 Sequence: 1 MNHLPPDMENALTGSSQSH.....EAGSEAEKQDEKPLEL 234
 Scoring table: BLOSUM62
 Gapop 10.0, Gapext 0.5
 Searched: 2105692 seqs, 386760381 residues
 Total number of hits satisfying chosen parameters: 2105692
 Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 1500 summaries

Database :
 1: geneseqp1980s:*
 2: geneseqp1990s:*
 3: geneseqp2000s:*
 4: geneseqp2001s:*
 5: geneseqp2002s:*
 6: geneseqp2003as:*
 7: geneseqp2003bs:*
 8: geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

No.	Score	Match	Length	DB	ID	Description
RESULT 1						
ID	AAU29056	standard;	protein;	234	AA.	
DE	Human PRO polypeptide sequence #33.					
PD	20-SEP-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1195;	DB 4;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 2						
ID	AAM39929	standard;	protein;	234	AA.	
DE	Human polypeptide SEQ ID NO 3074.					
PD	26-JUL-2001.					
PA	(HYSE-) HYSEQ INC.					
Query Match	100.0%;	Score 1195;	DB 4;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 3						
ID	AAH87532	standard;	protein;	234	AA.	
DE	Human PRO1864.					
PD	08-MAR-2001.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1195;	DB 4;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 4						
ID	ABG5857	standard;	protein;	234	AA.	
DE	Human secreted/transmembrane protein PRO1864.					
PD	29-AUG-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1195;	DB 5;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 5						
ID	ABB4847	standard;	protein;	234	AA.	
DE	Human PRO1864 protein sequence SEQ ID NO:62.					
PD	03-JAN-2002.					
PA	(GETH) GENENTECH INC.					
Query Match	100.0%;	Score 1195;	DB 5;	Length 234;		
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;				
RESULT 6						
ID	ABB95453	standard;	protein;	234	AA.	

DE	Human angiogenesis related protein PRO1864 SEQ ID NO: 62.
PD	31-JAN-2002.
PA	(GETH) GENENTECH INC.
PA	(BAKE/) BAKER K P.
PA	(FERR/) FERRARA N.
PA	(GERB/) GERBER H.
PA	(GERR/) GERRITSEN M E.
PA	(GODD/) GODDARD A.
PA	(GODD/) GODOWSKI P J.
PA	(GURN/) GURNEY A L.
PA	(HILL/) HILLMAN K J.
PA	(MARS/) MARSTERS S A.
PA	(PANJ/) PAN J.
PA	(PRON/) PRONT N F.
PA	(STEP/) STEPHAN J F.
PA	(WATA/) WATANABE C K.
PA	(WILL/) WILLIAMS P M.
PA	(WOOD/) WOOD W I.
Query Match	100.0%; Score 1195; DB 5; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 7	
ID	ABU58432 standard; protein; 234 AA.
DE	Human PRO polypeptide #33.
PD	US2003027272-A1.
PD	06-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 8	
ID	ABU87980 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.
PD	US2003032127-A1.
PD	13-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 9	
ID	ABU84295 standard; protein; 234 AA.
DE	Human secreted/transmembrane protein (PRO) #33.
PD	US2003032112-A1.
PD	13-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 10	
ID	ABR66169 standard; protein; 234 AA.
DE	Human secreted polypeptide PRO1864, SEQ ID NO:66.
PD	US2003027278-A1.
PD	06-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 11	
ID	ABR65559 standard; protein; 234 AA.
DE	Human secreted polypeptide PRO1864, SEQ ID NO:66.
PD	US2003036159-A1.
PD	20-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 12	
ID	ABU99499 standard; protein; 234 AA.
DE	Human secreted/transmembrane protein (PRO) #33.
PD	US2003040070-A1.
PD	27-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 13	
ID	ABU82738 standard; protein; 234 AA.
DE	Human PRO polypeptide #33.
PD	US2003032113-A1.
PD	13-FEB-2003.
Query Match	100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity	100.0%; Pred. No. 1.3e-131;
RESULT 14	
ID	ABU89859 standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.

PN US2003036147-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 15
ID ABR68108 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027264-A1.
06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 16
ID ABU96161 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036144-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 17
ID ABU92592 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036149-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 18
ID ABO08669 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044923-A1.
06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 19
ID ABO02721 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040062-A1.
27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 20
ID ABR74875 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040056-A1.
27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 21
ID ABR94637 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044926-A1.
06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 22
ID ABU85610 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036140-A1.
20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 23
ID ABU98770 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003013153-A1.
16-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 24
ID ABU97985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003017544-A1.
23-JAN-2003.

Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 25
ID ABU91691 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003027277-A1.
06-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 26
ID ABU89384 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036141-A1.
20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 27
ID ABU86225 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036146-A1.
20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 28
ID ABU67438 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036162-A1.
20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 29
ID ABU80466 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036137-A1.
20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 30
ID ABU90882 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018173-A1.
23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 31
ID ABO33941 standard; protein; 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2003090913-A1.
09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 32
ID ABR93984 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040063-A1.
27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 33
ID ABR98774 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040064-A1.
27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
RESULT 34
ID ABO16297 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.


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PN US2003027267-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 35
ID ABR92197 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036160-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 36
ID ABO1838 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044925-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 37
ID ABR78259 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054474-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 38
ID ABR3937 standard; protein; 234 AA.
DE Human prostate selective polypeptide P2340.
PN WO2003014298-A2.
PD 20-FEB-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 39
ID ABO171958 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003018183-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 40
ID ABO84995 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032114-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 41
ID ABO00134 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032101-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 42
ID ABO11466 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036124-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 43
ID ABO02111 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040054-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 44
ID ABO8685 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036133-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 45
ID ABO83380 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036134-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 46
ID ABO06181 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022294-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 47
ID ABR59217 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027275-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 48
ID ABO09279 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027324-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 49
ID ABO19143 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036118-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 50
ID ABO11161 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036123-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 51
ID ABR66779 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036148-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 52
ID ABO15992 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040060-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 53
ID ABO13698 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044916-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 54
ID ABO71512 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003013855-A1.
PD 16-JAN-2003.
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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 55
ID ABU65601 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, SEQ ID 66.
PN US2003036156-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 56
ID ABO07449 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032117-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 57
ID ABO03636 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036128-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 58
ID ABR67084 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027266-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 59
ID ABO15687 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054483-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 60
ID ABU55968 standard; protein; 234 AA.
DE Human secreted/transmembrane protein, PRO1864.
PN US2003022298-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 61
ID ABU72293 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2002182638-A1.
PD 05-DEC-2002.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 62
ID ABU65296 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032102-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 63
ID ABU95241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036117-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 64
ID ABU71144 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003036143-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 65
ID ABO07754 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032130-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 66
ID ABR69995 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032138-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 67
ID ABR69328 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036132-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 68
ID ABO01469 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003008353-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 69
ID ABU81271 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017542-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 70
ID ABR60068 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032137-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 71
ID ABR58287 standard; protein; 234 AA.
DE BC00092 protein #SEQ ID 20.
PN WO2003029421-A2.
PD 10-APR-2003.
PA (ORIG-) ORIGENE TECHNOLOGIES INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 72
ID ABU90966 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003018168-A1.
PD 23-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 73
ID ABR67803 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027269-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 74
ID ABR65191 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027268-A1.
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PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 75
ID ABR6413 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027274-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 76
ID ABR71825 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032135-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 77
ID ABR85305 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022295-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 78
ID ABR86995 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003022297-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 79
ID ABR83075 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032105-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 80
ID ABR94931 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032123-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 81
ID ABR90479 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032108-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 82
ID ABR93990 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032111-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 83
ID ABR93641 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032119-A1.
PD 13-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 84
ID ABR6486 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027263-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 85
ID ABR02787 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO1864.
PN US2003009012-A1.
PD 09-JAN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 86
ID ABR68718 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027271-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 87
ID ABR06534 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036125-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 88
ID ABR99079 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040068-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 89
ID ABR56963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027280-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 90
ID ABR85915 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022300-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 91
ID ABR82202 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036136-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 92
ID ABR87213 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036138-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 93
ID ABR83685 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032109-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 94
ID ABR08059 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003040066-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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RESULT 95
ID ABU92482 standard; protein: 234 AA.
DE Human secreted/transmembrane protein PRO1864.
PN US2003045684-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 96
ID ABU81770 standard; protein: 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032104-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 97
ID ABU65934 standard; protein: 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036157-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 98
ID ABU81152 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864.
PN US2003027212-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 99
ID ABR59763 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032120-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 100
ID ABU93951 standard; protein: 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036155-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 101
ID ABU99804 standard; protein: 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003022296-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 102
ID ABR66474 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027281-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 103
ID ABR90892 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040058-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 104
ID ABO5367 standard; protein: 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003027986-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 105
ID ABU94319 standard; protein: 234 AA.
DE Human PRO polypeptide #33.
PN US2003017540-A1.
PD 23-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 106
ID ABU79401 standard; protein: 234 AA.
DE Human PRO polypeptide #33.
PN US2003032106-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 107
ID ABU86530 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032129-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 108
ID ABU86635 standard; protein: 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032131-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 109
ID ABU94624 standard; protein: 234 AA.
DE Human PRO polypeptide #33.
PN US2003032103-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 110
ID ABO04551 standard; protein: 234 AA.
DE Human PRO polypeptide #33.
PN US2003032107-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 111
ID ABR70300 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032139-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 112
ID ABU98465 standard; protein: 234 AA.
DE Human PRO polypeptide #33.
PN US2003022301-A1.
PD 30-JAN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 113
ID ABR65864 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036165-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 114
ID ABR64581 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027262-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 115

ID ABU79506 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032110-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU72697 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036142-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU95856 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036145-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU91076 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036154-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU90169 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036153-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABO0584 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044931-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABO1085 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036150-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABR70910 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040069-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABO98269 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183493-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU87518 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003022293-A1.
PD 30-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU91386 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032128-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU9274 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003036634-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU84600 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032116-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABR63690 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032122-A1.
PD 13-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU80067 standard; protein; 234 AA.
DE Human PRO protein #33.
PN US2003036139-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU82481 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2002183494-A1.
PD 05-DEC-2002.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU93336 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003017541-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABO09889 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003017543-A1.
PD 23-JAN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABO08974 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036152-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU96445 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003027993-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
Pred. No. 1.3e-131;
ID ABU10542 standard; protein; 234 AA.
DE Human secreted/transmembrane protein #33.

PN US2002127584-A1.
PD 12-SEP-2002.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 136
ID ABU72115 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003023042-A1.
PD 30-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 137
ID ABU95551 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003032115-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 138
ID ABU96760 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003032140-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 139
ID ABR70605 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040076-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 140
ID ABO04956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003008352-A1.
PD 09-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 141
ID ABO08364 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044922-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 142
ID ABO05571 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032118-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 143
ID ABR73960 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036135-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 144
ID ABR95552 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054455-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 145

ID ABR80849 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049741-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 146
ID ABR81154 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049743-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 147
ID ABM00850 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049769-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 148
ID ABR8452 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068743-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 149
ID ABW7273 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054479-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 150
ID ABO28757 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068685-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 151
ID ABO31502 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068725-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 152
ID ABM07919 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068752-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 153
ID ABO40399 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068682-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 154
ID ABO35824 standard; protein; 234 AA.

DE Human PRO polypeptide #33.
PN US2003068701-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 155
ID ABO43963 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068755-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 156
ID ADA77818 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073180-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 157
ID ABM24758 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104539-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 158
ID ABO03026 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036131-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 159
ID ABR90282 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040075-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 160
ID AM17196 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054459-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 161
ID ABR94942 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044930-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 162
ID ABR95247 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040071-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 163
ID ADB17071 standard; protein; 234 AA.
DE Human transmembrane PRO polypeptide (Segid 14).
PN US2003050462-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 164
ID ABO21485 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054471-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 165
ID ABR97749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064452-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 166
ID ABR87537 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068705-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 167
ID ABM77578 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054473-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 168
ID ABM27808 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064440-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 169
ID ABM06089 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068704-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 170
ID ABM03595 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068722-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 171
ID ABM35046 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073183-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 172
ID ABM26283 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104549-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 173

[illegible]

DE	Human secreted polypeptide PRO1864,	SEQ ID NO:66.
PN	US2003068707-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 183		
ID	ABM09444 standard; protein; 234 AA.	
DE	Human secreted polypeptide PRO1864,	SEQ ID NO:66.
PN	US2003073175-A1.	
PD	17-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 184		
ID	ABO41314 standard; protein; 234 AA.	
DE	Human secreted/transmembrane protein (PRO) #33.	
PN	US2003068695-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 185		
ID	ABO36129 standard; protein; 234 AA.	
DE	Human PRO polypeptide #33.	
PN	US2003068703-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 186		
ID	ABO43658 standard; protein; 234 AA.	
DE	Human PRO polypeptide #33.	
PN	US2003068732-A1.	
PD	10-APR-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 187		
ID	ABM76358 standard; protein; 234 AA.	
DE	Human secreted polypeptide PRO1864,	SEQ ID NO:66.
PN	US2003082717-A1.	
PD	01-MAY-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 188		
ID	ABM76054 standard; protein; 234 AA.	
DE	Human secreted polypeptide PRO1864,	SEQ ID NO:66.
PN	US2003104548-A1.	
PD	05-JUN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 189		
ID	ABM25673 standard; protein; 234 AA.	
DE	Human secreted polypeptide PRO1864,	SEQ ID NO:66.
PN	US2003104542-A1.	
PD	05-JUN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 190		
ID	ABM25978 standard; protein; 234 AA.	
DE	Human secreted polypeptide PRO1864,	SEQ ID NO:66.
PN	US2003104543-A1.	
PD	05-JUN-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#
ID	Best Local Similarity	Pred. No. 1.3e-131;
RESULT 191		
ID	ABO03331 standard; protein; 234 AA.	
DE	Human secreted/transmembrane protein (PRO) #33.	
PN	US2003036127-A1.	
PD	20-FEB-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 6;	Length 234#

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 192
ID ABO02416 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040061-A1.
PD 27-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 193
ID ABO44245 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003018172-A1.
PD 23-JAN-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 194
ID ABR90587 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036130-A1.
PD 20-FEB-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 195
ID ABR73655 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054468-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 196
ID ABO16907 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054470-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 197
ID ABR94332 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044917-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 198
ID ABR75839 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044929-A1.
PD 06-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 199
ID ABR71215 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059880-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 200
ID ABR93112 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064465-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 201
ID ABR93417 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054478-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 202
ID ABR87842 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068718-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 203
ID ABO27842 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064454-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 204
ID ABO29977 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064461-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 205
ID ABO33186 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068724-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 206
ID ABO44874 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068727-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 207
ID ABO8834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068772-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 208
ID ABO36434 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068714-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 209
ID ABO35519 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068758-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 210
ID ABO39484 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068776-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 211
ID ABL10359 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003069407-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 212
ID ABL11884 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104555-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 213
ID ABO52030 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049768-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 214
ID ABO52335 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049771-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 215
ID ABL19876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003069394-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 216
ID ABO23653 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032134-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 217
ID ABL17259 standard; protein; 234 AA.
DE Human transmembrane PRO polypeptide (SeqID 14).
PN US2003050465-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 218
ID ABL97139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054481-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 219
ID ABL86927 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049778-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
Query Match 100.0%; Score 1195; DB 6; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 220
ID ABL10969 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049782-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 221
ID ABL28113 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054476-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 222
ID ABO32112 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068733-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 223
ID ABL15239 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068692-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 224
ID ABL06394 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068709-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 225
ID ABL04205 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068716-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 226
ID ABL22318 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068740-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 227
ID ABL07614 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068751-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 228
ID ABL040704 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068684-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
Query Match 100.0%; Score 1195; DB 6; Length 234;

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RESULT 229
ID ABM35351 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073179-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 230
ID ABM33114 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087374-A1.
PD 08-MAY-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 231
ID ABOS2640 standard; protein: 234 AA.
DE Human PRO polypeptide #33.
PN US2003049773-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 232
ID ABO50200 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003048777-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 233
ID ABU99194 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040055-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 234
ID ABO04246 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036164-A1.
PD 20-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 235
ID ABO05876 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040074-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 236
ID AM18416 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054480-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 237
ID ABR97444 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059885-A1.
PD 27-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 238
ID ABR80544 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049740-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 239
ID ABM01155 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049770-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 240
ID ABR88757 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073169-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 241
ID ABM13409 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064457-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 242
ID ABM20793 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068711-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 243
ID ABO41924 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049745-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 244
ID ABO42534 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003048751-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 245
ID ABM10054 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003067478-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 246
ID ABO38569 standard; protein: 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068773-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 247
ID ABM32809 standard; protein: 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073185-A1.
PD 17-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 248
ID ABM22623 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003087373-A1.
PD 08-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
PD 10-APR-2003.
ID ABM74834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096353-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 250
ID ADH79610 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073173-A1.
PD 17-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 251
ID ABR96224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054458-A1.
PD 20-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 252
ID ABM02375 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059886-A1.
PD 27-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 253
ID ABR86317 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049758-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 254
ID ABR86622 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049772-A1.
PD 13-MAR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 255
ID ABM16586 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064448-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 256
ID ABM29638 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064456-A1.
PD 03-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 257
ID ABO29062 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068693-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 258
ID ABM23843 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068735-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 259
ID ABM23233 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068753-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 260
ID ABM22013 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068742-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 261
ID ABO37654 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068756-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 262
ID ABM28418 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003082715-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 263
ID ABM28723 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003082716-A1.
PD 01-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 264
ID ABM66367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068737-A1.
PD 10-APR-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 265
ID ABM75749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104547-A1.
PD 05-JUN-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
RESULT 266
ID ABM34029 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096359-A1.
PD 22-MAY-2003.
Query Match
Best Local Similarity 100.0%; Score 1195; DB 6; Length 234;
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Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 267
ID ABO4334 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US200310061-A1.
PD 29-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 268
ID ABO20265 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032125-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 269
ID ABO21180 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054454-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 270
ID ABO22095 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054477-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 271
ID ADA20048 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003055222-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 272
ID ABO34173 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.
PN US2003060601-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 273
ID ABR96529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054460-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 274
ID ABR85707 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049753-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 275
ID ABR9689 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049763-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 276
ID ABO00545 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 277
ID ABO00240 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073172-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 278
ID ABO23672 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068700-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 279
ID ABO23538 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068736-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 280
ID ABO23933 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068799-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 281
ID ABO38264 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068767-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 282
ID ABO45564 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003073182-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 283
ID ABO20488 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104557-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 284
ID ADA81337 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003092121-A1.
PD 15-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 285
ID ABO16602 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003027276-A1.
PD 06-FEB-2003.

Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 286
ID ABO18228 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044920-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 287
ID ABO22655 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003027265-A1.
PD 06-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 288
ID ABO22960 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054461-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 289
ID ABR92502 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064446-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 290
ID ABR81459 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049744-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 291
ID ABM77883 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049783-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 292
ID ABR89672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073171-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 293
ID ABM26588 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032121-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 294
ID ABM13714 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064458-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 295
ID ABO28452 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.

PN US2003064460-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 296
ID ABO30282 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064464-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 297
ID ABM07309 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068702-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 298
ID ABM03900 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068734-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 299
ID ABO37044 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068719-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 300
ID ABO41619 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068729-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 301
ID ABO35214 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068738-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 302
ID ABM25063 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104540-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 303
ID ABO47455 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049742-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 304
ID ABO47760 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049747-A1.
PD 13-MAR-2003.

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PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 305
ID ABO48370 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049750-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 306
ID ABO51420 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049766-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 307
ID ABO51725 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049767-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 308
ID ABO50505 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049779-A1.
PD 13-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 309
ID ABR79629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003040059-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 310
ID ABM16891 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003040078-A1.
PD 27-FEB-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 311
ID ABO17923 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044918-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 312
ID ABO20875 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032132-A1.
PD 13-FEB-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 313
ID ABR96834 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003054462-A1.
PD 20-MAR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 314
ID ABM12189 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003064445-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 315
ID ABM16281 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003064449-A1.
PD 03-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 316
ID ABM24148 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003064441-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 317
ID ABM14629 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003068696-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 318
ID ABM04510 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003068712-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 319
ID ABM0669 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003068730-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 320
ID ABM09139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003073174-A1.
PD 17-APR-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 321
ID ABO39179 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068775-A1.
PD 10-APR-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 322
ID ABM75444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003104545-A1.
PD 05-JUN-2003.
PA (GETH ) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 323
ID ABM25368 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1664, SEQ ID NO:66.
PN US2003104541-A1.
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PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 324
ID ABM19678 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104554-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 325
ID ABO46784 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049762-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 326
ID ABO47089 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049765-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 327
ID ADA83135 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049752-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 328
ID ABR71520 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032133-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 329
ID ABR72130 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032136-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 330
ID ABR98469 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003032139-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 331
ID ABO06839 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040053-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 332
ID ABR84792 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040057-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 333
ID ABR73350 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.

PN US2003054467-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 334
ID ABR76444 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044932-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 335
ID ABR73045 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027270-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 336
ID ABM18111 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054469-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 337
ID ABO20570 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032126-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 338
ID ABO25313 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054463-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 339
ID ABO25618 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003054466-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 340
ID ABR94027 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059879-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 341
ID ABR79934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049738-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 342
ID ABM1274 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064469-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 343
ID ABO32881 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003064453-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 344
ID ABO30587 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 345
ID ABO30892 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064466-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 346
ID ABM27198 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068760-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 347
ID ABM29943 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068769-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 348
ID ABM05479 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003045700-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 349
ID ABM15544 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068698-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 350
ID ABM08529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068759-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 351
ID ABO42229 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049748-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 352
ID ABO0345 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.

ID ABO37959 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068765-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 353
ID ABO45869 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049754-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 354
ID ABM6672 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068688-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 355
ID ADB20178 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003082767-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 356
ID ABM19573 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104552-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 357
ID ABO49285 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049774-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 358
ID ABO49590 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049775-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 359
ID ABO78430 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003073181-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 360
ID ABR88147 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068720-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 361
ID ADA00345 standard; protein; 234 AA.
DE Human secreted/transmembrane polypeptide PRO 1864.

PN US2003027992-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 362
ID AM26893 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068739-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 363
ID AM03290 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068763-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 6; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 364
ID ABO39789 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068689-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 365
ID ABO49895 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049776-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 366
ID ABO50810 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049780-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 367
ID ABO05266 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036126-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 368
ID ABR74570 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044924-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 369
ID ABR77049 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044927-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 370
ID ABM17806 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040072-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 371
ID ABR95857 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040073-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 372
ID ABO21790 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054475-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 373
ID ABO19960 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003032124-A1.
PD 13-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 374
ID ABO24263 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064467-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 375
ID ABR86012 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049759-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 376
ID ABM10664 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064455-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 377
ID ABM76663 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054465-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 378
ID ABR89367 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073170-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 379
ID ABM12494 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073176-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 380
ID ABM05784 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068717-A1.

PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 381
ID ABO34909 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003068728-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 382
ID ABM02985 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068764-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 383
ID ABM18963 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104550-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 384
ID ABM19268 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104551-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 385
ID ABO46479 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049761-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 386
ID ABO46980 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049757-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 387
ID ABR69023 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003027273-A1.
PD 06-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 388
ID ABR89062 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036119-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 389
ID ABR72435 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036120-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 390
ID ABR74265 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036161-A1.
PD 20-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 391
ID ABO18533 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044921-A1.
PD 06-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 392
ID ABR80239 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049739-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 393
ID ABM01460 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059882-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 394
ID ABM02070 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059884-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 395
ID ABR87232 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068687-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 396
ID ABM12799 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073186-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 397
ID ABM30553 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064443-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 398
ID ABM24453 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064444-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 399
ID ABO29367 standard; protein; 234 AA.

DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068697-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 400
ID ABO31197 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068710-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 401
ID ABO114324 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068686-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 402
ID ABO09749 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073178-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 403
ID ABO38874 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068774-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 404
ID ABO34639 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104538-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 405
ID ABO5115 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049781-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 406
ID ABO03941 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036158-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 407
ID ABO10411 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003036151-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 408
ID ABR77654 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040067-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 409
ID ABR78864 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054456-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 410
ID ABO23958 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054482-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 411
ID ABR93722 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054457-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 412
ID ABO11765 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003059883-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 413
ID ABO78188 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049764-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 414
ID ABR8977 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003073177-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 415
ID ABO27503 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064442-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 416
ID ABO11304 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003064450-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 417
ID ABO31807 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068731-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 418

ID ABO14019 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068683-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 419
ID ABO18224 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068754-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 420
ID ABO40094 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068681-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 421
ID ABO74529 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096351-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 422
ID ABO33724 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096358-A1.
PD 22-MAY-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 423
ID ABO20183 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104556-A1.
PD 05-JUN-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 424
ID ABO48675 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049756-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 425
ID ABO72740 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003036122-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 426
ID ABO15382 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003036121-A1.
PD 20-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 427
ID ABO85097 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003040065-A1.
PD 27-FEB-2003.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 428
ID ABO15077 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003044919-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 429
ID ABO1712 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003040077-A1.
PD 27-FEB-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 430
ID ABO17501 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003044928-A1.
PD 06-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 431
ID ABO85402 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003049746-A1.
PD 13-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 432
ID ABO7668 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003054464-A1.
PD 20-MAR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 433
ID ABO28147 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003064459-A1.
PD 03-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 434
ID ABO22928 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068757-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 435
ID ABO30248 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068723-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 436
ID ABO21708 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068741-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 437
ID ABO21403 standard; protein; 234 AA.

DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068744-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 438
ID ABM14934 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068766-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 439
ID ABO41009 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068694-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 440
ID ABO36739 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068715-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 441
ID ABO37349 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003068726-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 442
ID ABM75139 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003104544-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 443
ID ABM33419 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003096357-A1.
PD 22-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 444
ID ABO46174 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003049760-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 445
ID ADA82501 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003049755-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 446
ID ADB85687 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.

PN US2003049735-A1.
PD 13-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 447
ID ABM31773 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068680-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 448
ID ABM31163 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068762-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 449
ID ADB85609 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003054472-A1.
PD 20-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 450
ID ABM32078 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068708-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 451
ID ABM32383 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068713-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 452
ID ADB68266 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003065161-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 453
ID ADB68073 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003060600-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 454
ID ABM31468 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068761-A1.
PD 10-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 455
ID ABM30858 standard; protein; 234 AA.
DE Human secreted polypeptide PRO1864, SEQ ID NO:66.
PN US2003068771-A1.
PD 10-APR-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 456
ID ADB90890 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003083473-A1.
PD 01-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 457
ID ADC06970 standard; protein; 234 AA.
DE Human PRO1864 protein.
PN US2003060602-A1.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 458
ID ADC17149 standard; protein; 234 AA.
DE Mammalian PRO polypeptide (Seqid 14).
PN US2003065143-A1.
PD 03-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 459
ID ADC1847 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073208-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 460
ID ADC52342 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003138882-A1.
PD 24-JUL-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 461
ID ADD05539 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003087376-A1.
PD 08-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 462
ID ADD10351 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105011-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 463
ID ADD11311 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105013-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 464
ID ADD37104 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003105012-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 465
ID ADD36018 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003105298-A1.
PD 05-JUN-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 466
ID ADG01019 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003078387-A1.
PD 24-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 467
ID ADG08572 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180793-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 468
ID ADG02534 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207397-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 469
ID ADG01241 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207399-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 470
ID ADF95416 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207398-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 471
ID ADF95193 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180795-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 472
ID ADG12231 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207392-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 473
ID ADH24046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180918-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;

RESULT 474
ID ADH34072 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180858-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 475
ID ADH29905 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180859-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 476
ID ADH2376 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180919-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 477
ID ADH08891 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003207395-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 478
ID ADG8580 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180904-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 479
ID ADH2456 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180907-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 480
ID ADH37412 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181646-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 481
ID ADH02001 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180837-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 482
ID ADH37582 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181648-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 483

ID ADG85620 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180905-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 484
ID ADH24216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180914-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 485
ID ADH38510 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181643-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 486
ID ADG83631 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180794-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 487
ID ADH29439 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180860-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 488
ID ADH2755 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180906-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 489
ID ADH37752 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181647-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 490
ID ADH37929 standard; protein; 234 AA.
DE Human secreted and transmembrane protein PRO1864.
PN US2003181649-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 491
ID ADH57349 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180920-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 492
ID ADH53491 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181636-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 493
ID ADH53661 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181641-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 494
ID ADH51997 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181638-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 495
ID ADH49852 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181639-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 496
ID ADI25362 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181696-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 497
ID ADH90155 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181698-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 498
ID ADI25532 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181669-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 499
ID ADH9706 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181672-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 500
ID ADI03554 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181656-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 501
ID ADI11911 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181654-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 502
ID ADH89985 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181697-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 503
ID ADH98386 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181707-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 504
ID ADI11061 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181682-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 505
ID ADI11571 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181684-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 506
ID ADH98216 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181709-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 507
ID ADH98556 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181708-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 508
ID ADH98046 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181673-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 509
ID ADI05034 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180848-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 510
ID ADI03384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181654-A1.

PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 511
ID AD104779 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181657-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 512
ID ADH78233 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181668-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 513
ID AD119577 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181676-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 514
ID ADH90325 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181699-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 515
ID AD103044 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181653-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 516
ID ADH77893 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181666-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 517
ID ADH97876 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181674-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 518
ID AD101261 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190669-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 519
ID AD101956 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181652-A1.
PD 25-SEP-2003.

PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 520
ID AD103214 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181655-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 521
ID AD111401 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181681-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 522
ID AD102303 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181650-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 523
ID AD111741 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181685-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 524
ID AD105378 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003190716-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 525
ID ADH79450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191290-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 526
ID AD119407 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181675-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 527
ID AD105208 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181677-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 528
ID ADH79620 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191288-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.

Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 529
ID AD101446 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181678-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 530
ID AD101616 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181679-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 531
ID AD101786 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181680-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 532
ID ADH79790 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191289-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 533
ID AD104608 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003171550-A1.
PD 11-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 534
ID AD102744 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181651-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 535
ID ADH78063 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181667-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 536
ID AD125702 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181670-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 537
ID AD125672 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181671-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 547

Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 538
ID ADK65384 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073821-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 539
ID ADH98726 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191284-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 540
ID ADH79967 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003191287-A1.
PD 09-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 541
ID ADL32672 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003207396-A1.
PD 06-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 542
ID ADM30206 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003073813-A1.
PD 17-APR-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 543
ID ADL93698 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003040013-A1.
PD 27-FEB-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 7; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 544
ID ADC52152 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003104947-A1.
PD 28-MAY-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 545
ID ADE41312 standard; protein; 234 AA.
DE Human secreted/transmembrane PRO polypeptide #31.
PN US2003100497-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 546
ID ADE74203 standard; protein; 234 AA.
DE Human secreted/transmembrane protein (PRO) #33.
PN US2003211572-A1.
PD 13-NOV-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 547

ID AD874815 standard; protein; 234 AA.
DE Human secreted/cransmembrane protein (PRO) #33.
PN US2003211574-A1.
PD 13-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 548
ID ADP96028 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215909-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 549
ID ADG04299 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215912-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 550
ID ADG00459 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003215911-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 551
ID ADH06584 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180852-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 552
ID ADH06414 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180853-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 553
ID ADG68635 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180855-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 554
ID ADH27725 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180912-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 555
ID ADH25066 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180913-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 556
ID ADH33698 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003181645-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 557
ID ADG82715 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2003215910-A1.
PD 20-NOV-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 558
ID ADH02341 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180839-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 559
ID ADH07948 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180845-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 560
ID ADG69345 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180846-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 561
ID ADH39166 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180917-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 562
ID ADH25996 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003068770-A1.
PD 10-APR-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 563
ID ADG83906 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003180842-A1.
PD 25-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 564
ID ADG85450 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003166848-A1.
PD 04-SEP-2003.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 565
ID ADH06244 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003180854-A1.
PD 25-SEP-2003.

PA	(GETH) GENENTECH INC.	100.0%;	Score 1195;	DB 8;	Length 234;
Query Match					
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 566					
ID	ADH30074 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
FN	US2003180856-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 567					
ID	ADH24396 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
FN	US2003180910-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 568					
ID	ADH32965 standard; protein; 234 AA.				
DE	Human PRO polypeptide #33.				
FN	US2003068768-A1.				
PD	10-APR-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 569					
ID	ADG65915 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
FN	US2003180844-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 570					
ID	ADH07778 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
FN	US2003180851-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 571					
ID	ADG65790 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
FN	US2003180861-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 572					
ID	ADH39336 standard; protein; 234 AA.				
DE	Novel human secreted and transmembrane protein PRO1864.				
FN	US2003180916-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 573					
ID	ADH35528 standard; protein; 234 AA.				
DE	Human PRO polypeptide #7.				
FN	US2003181637-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 574					
ID	ADH33868 standard; protein; 234 AA.				
DE	Human PRO polypeptide #7.				
FN	US2003181644-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				
Query Match		100.0%;	Score 1195;	DB 8;	Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;		
RESULT 575					
ID	ADH33868 standard; protein; 234 AA.				
DE	Human PRO polypeptide #7.				
FN	US2003181644-A1.				
PD	25-SEP-2003.				
PA	(GETH) GENENTECH INC.				

ID	ADH01078	standard; protein; 234 AA.
DE	Human PRO polypeptide #7.	
PN	US2003180638-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
RESULT 576		
ID	ADG69685	standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180843-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
RESULT 577		
ID	ADH02171	standard; protein; 234 AA.
DE	Human PRO polypeptide #7.	
PN	US2003180841-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
RESULT 578		
ID	ADG69175	standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180847-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
RESULT 579		
ID	ADG85960	standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180862-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
RESULT 580		
ID	ADH24896	standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180909-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
RESULT 581		
ID	ADH39513	standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180915-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
RESULT 582		
ID	ADH02511	standard; protein; 234 AA.
DE	Human PRO polypeptide #7.	
PN	US2003180840-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
RESULT 583		
ID	ADG69005	standard; protein; 234 AA.
DE	Novel human secreted and transmembrane protein PRO1864.	
PN	US2003180849-A1.	
PD	25-SEP-2003.	
PA	(GETH) GENENTECH INC.	
Query Match	100.0%; Score 1195; DB 8; Length 234;	
Beet Local Similarity	100.0%; Pred. No. 1.3e-131;	
Query Match	100.0%; Score 1195; DB 8; Length 234;	

Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 584		
ID ADH07608 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003180850-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 585		
ID ADG6130 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003180863-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 586		
ID ADH24726 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003180908-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 587		
ID ADH25774 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003180911-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 588		
ID ADH38340 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003180922-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 589		
ID ADH57179 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003181642-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 590		
ID ADH43495 standard; protein; 234 AA.		
DE Novel human PRO polypeptide #31.		
FN US2003224984-A1.		
PD 04-DEC-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 591		
ID ADHS2167 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003180921-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 592		
ID ADH49533 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003180857-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;
RESULT 593		
ID ADH49533 standard; protein; 234 AA.		
DE Novel human secreted and transmembrane protein PRO1864.		
FN US2003180857-A1.		
PD 25-SEP-2003.		
PA (GETH) GENENTECH INC.		
Query Match	100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity	100.0%;	Pred. No. 1.3e-131;

RESULT 593	ID	ADH90495	standard; protein; 234 AA.
DE	Novel	human secreted and transmembrane protein PRO1864.	
	PN	US2003181700-A1.	
	PD	25-SEP-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 594	ID	AD111231	standard; protein; 234 AA.
DE	Human PRO	polypeptide #7.	
	PN	US2003181683-A1.	
	PD	25-SEP-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 595	ID	ADH98896	standard; protein; 234 AA.
DE	Novel	human secreted and transmembrane protein PRO1864.	
	PN	US2003190698-A1.	
	PD	09-OCT-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 596	ID	AD102126	standard; protein; 234 AA.
DE	Novel	human secreted and transmembrane protein PRO1864.	
	PN	US2003190699-A1.	
	PD	09-OCT-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 597	ID	ADH90665	standard; protein; 234 AA.
DE	Novel	human secreted and transmembrane protein PRO1864.	
	PN	US2003181701-A1.	
	PD	25-SEP-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 598	ID	ADJ54704	standard; protein; 234 AA.
DE	Human PRO	polypeptide #33.	
	PN	US2004023321-A1.	
	PD	05-FEB-2004.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 599	ID	ADJ98540	standard; protein; 234 AA.
DE	Novel	human secreted and transmembrane protein PRO1864.	
	PN	US2003187197-A1.	
	PD	02-OCT-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 600	ID	ADJ98710	standard; protein; 234 AA.
DE	Novel	human secreted and transmembrane protein PRO1864.	
	PN	US2003187228-A1.	
	PD	02-OCT-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 601	ID	ADH78869	standard; protein; 234 AA.
DE	Novel	human secreted and transmembrane protein PRO1864.	
	PN	US2003181703-A1.	
	PD	25-SEP-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;
RESULT 602	ID	ADH78869	standard; protein; 234 AA.
DE	Novel	human secreted and transmembrane protein PRO1864.	
	PN	US2003181703-A1.	
	PD	25-SEP-2003.	
	PA	(GETH) GENENTECH INC.	
Query Match		100.0%;	Score 1195; DB 8; Length 234;
Best Local Similarity		100.0%;	Pred. No. 1.3e-131;

ID ADJ99103 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003186408-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 603
ID ADJ99273 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187196-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 604
ID ADJ98891 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187242-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 605
ID ADH79039 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003181702-A1.
PD 25-SEP-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 606
ID ADK00899 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2003186407-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 607
ID ADK14420 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2003187229-A1.
PD 02-OCT-2003.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 608
ID ADK82840 standard; protein; 234 AA.
DE Human PRO polypeptide #31.
PN US2004043927-A1.
PD 04-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 609
ID ADJ64475 standard; protein; 234 AA.
DE Human PRO polypeptide #33.
PN US2004038337-A1.
PD 26-FEB-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 610
ID ADM31371 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004048334-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 611
ID ADM36418 standard; protein; 234 AA.

DE Novel human secreted and transmembrane protein PRO1864.
PN US2004053358-A1.
PD 18-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 612
ID ADM40223 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004048335-A1.
PD 11-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 613
ID ADM80869 standard; protein; 234 AA.
DE Human PRO polypeptide #7.
PN US2004058411-A1.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 614
ID ADL91873 standard; protein; 234 AA.
DE Human PRO1864 protein SEQ ID NO:94.
PN WO2004024076-A2.
PD 25-MAR-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 615
ID ADN37831 standard; protein; 234 AA.
DE Novel human secreted and transmembrane protein PRO1864.
PN US2004091959-A1.
PD 13-MAY-2004.
PA (GETH) GENENTECH INC.
Query Match 100.0%; Score 1195; DB 8; Length 234;
Best Local Similarity 100.0%; Pred. No. 1.3e-131;
RESULT 616
ID AAM41716 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6647.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.4e-131;
RESULT 617
ID AAM41715 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 6646.
PN WO20015312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 100.0%; Score 1195; DB 4; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.4e-131;
RESULT 618
ID ABP75508 standard; protein; 238 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 692.
PN WO20028376-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 100.0%; Score 1195; DB 6; Length 238;
Best Local Similarity 100.0%; Pred. No. 1.4e-131;
RESULT 619
ID ABR58404 standard; protein; 234 AA.
DE Human NOV19D.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA) CURAGEN CORP.
Query Match 99.4%; Score 1188; DB 6; Length 234;
Best Local Similarity 99.6%; Pred. No. 8.9e-131;
RESULT 620
ID AAM39930 standard; protein; 216 AA.
DE Human polypeptide SEQ ID NO 3075.

PN WO200153312-A1.
ID 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 91.8%; Score 1097; DB 4; Length 216;
Best Local Similarity 92.3%; Pred. No. 4.1e-120;
RESULT 621
ID ABB90287 standard; protein; 201 AA.
DE Human polypeptide SEQ ID NO 2663.
PN WO200150304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 85.7%; Score 1024; DB 5; Length 201;
Best Local Similarity 100.0%; Pred. No. 1.4e-111;
RESULT 622
ID ABR58403 standard; protein; 198 AA.
DE Human NOV19a.
PN WO2003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match 82.4%; Score 985; DB 6; Length 198;
Best Local Similarity 84.6%; Pred. No. 5.4e-107;
RESULT 623
ID AAU30250 standard; protein; 283 AA.
DE Novel human secreted protein #741.
PN WO200179449-A2.
PD 25-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 65.0%; Score 777; DB 4; Length 283;
Best Local Similarity 72.5%; Pred. No. 2.6e-82;
RESULT 624
ID ADB64413 standard; protein; 176 AA.
DE Human protein encoded by clone FEBRA20007820.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
Query Match 56.0%; Score 669.5; DB 7; Length 176;
Best Local Similarity 87.5%; Pred. No. 6e-70;
RESULT 625
ID ADK36828 standard; protein; 146 AA.
DE Novel human polypeptide SeqID8910.
PN WO200216439-A2.
PD 28-FEB-2002.
PA (HYSE-) HYSEQ INC.
Query Match 55.6%; Score 665; DB 5; Length 146;
Best Local Similarity 91.0%; Pred. No. 1.6e-69;
RESULT 626
ID AAM25768 standard; protein; 445 AA.
DE Human MLN 64.
PN WO9706256-A2.
PD 20-FEB-1997.
PA (INRM) INST NAT SANTE & RECH MEDICALE.
PA (CNRS) CENT NAT RECH SCI.
PA (UYPA-) UNIV PASTEUR LOUIS.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 55.6%; Score 664; DB 2; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.6e-69;
RESULT 627
ID ABR47530 standard; protein; 445 AA.
DE Breast cancer associated protein sequence SEQ ID NO:296.
PN WO200304989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 55.6%; Score 664; DB 6; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.6e-69;
RESULT 628
ID ADH13184 standard; protein; 445 AA.
DE Human malignant neoplasia-related protein SeqID33.
PN EPI365034-A2.
PD 26-NOV-2003.
PA (FARB) BAYER AG.
Query Match 55.6%; Score 664; DB 8; Length 445;
Best Local Similarity 56.2%; Pred. No. 9.6e-69;

RESULT 629
ID ABB05498 standard; protein; 534 AA.
DE Novel human diagnostic protein #5489.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 52.3%; Score 625; DB 4; Length 534;
Best Local Similarity 48.9%; Pred. No. 4.8e-64;
RESULT 630
ID ABR69622 standard; protein; 412 AA.
DE Human CGPD-22 protein.
PN WO2003027263-A2.
PD 03-APR-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 48.4%; Score 578; DB 6; Length 412;
Best Local Similarity 58.3%; Pred. No. 1.1e-58;
RESULT 631
ID ABR75900 standard; protein; 111 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1084.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 33.9%; Score 405.5; DB 6; Length 111;
Best Local Similarity 73.7%; Pred. No. 3.6e-39;
RESULT 632
ID ABR59968 standard; protein; 580 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6696.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 28.7%; Score 343; DB 4; Length 580;
Best Local Similarity 37.8%; Pred. No. 8e-31;
RESULT 633
ID AAM90384 standard; protein; 70 AA.
DE Human immune/haematopoietic antigen SEQ ID NO:17977.
PN WO200157182-A2.
PD 09-AUG-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 26.9%; Score 322; DB 4; Length 70;
Best Local Similarity 98.4%; Pred. No. 1.3e-29;
RESULT 634
ID AAB96637 standard; protein; 424 AA.
DE Putative P. abyssi nucleoside-diphosphate-sugar pyrophosphorylase #6.
PN FR2792651-A1.
PD 27-OCT-2000.
PA (CNRS) CNRS CENT NAT RECH SCI.
PA (IFRE-) IFREMER INST FR RECH EXPL MER.
Query Match 7.8%; Score 93.5; DB 4; Length 424;
Best Local Similarity 21.9%; Pred. No. 0.12;
RESULT 635
ID AAU03699 standard; protein; 373 AA.
DE Group B streptococcus antigenic protein, ID-176.
PN WO200132882-A2.
PD 10-MAY-2001.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 7.6%; Score 91; DB 4; Length 373;
Best Local Similarity 25.7%; Pred. No. 0.19;
RESULT 636
ID ABB30317 standard; protein; 651 AA.
DE Streptococcus polypeptide SEQ ID NO 9810.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%; Score 91; DB 5; Length 651;
Best Local Similarity 25.7%; Pred. No. 0.42;
RESULT 637
ID ABB29732 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 8640.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.

Query Match 7.6%; Score 91; DB 5; Length 654;
Best Local Similarity 25.7%; Pred. No. 0.42;
RESULT 638
ID ABB26469 standard; protein; 654 AA.
DE Streptococcus polypeptide SEQ ID NO 2114.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 7.6%; Score 91; DB 5; Length 654;
Best Local Similarity 25.7%; Pred. No. 0.42;
RESULT 639
ID AAG61678 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 80037.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 87.5; DB 3; Length 155;
Best Local Similarity 21.4%; Pred. No. 0.15;
RESULT 640
ID AAG59838 standard; protein; 155 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77441.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.3%; Score 87.5; DB 3; Length 155;
Best Local Similarity 21.4%; Pred. No. 0.15;
RESULT 641
ID AAB58945 standard; protein; 516 AA.
DE Breast and ovarian cancer associated antigen protein sequence SEQ ID 653.
PN W0200055173-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 7.3%; Score 87.5; DB 3; Length 516;
Best Local Similarity 25.2%; Pred. No. 0.78;
RESULT 642
ID ADO39266 standard; protein; 421 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 929.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.3%; Score 87; DB 8; Length 421;
Best Local Similarity 23.7%; Pred. No. 0.67;
RESULT 643
ID ADO39263 standard; protein; 223 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 926.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 223;
Best Local Similarity 25.5%; Pred. No. 0.42;
RESULT 644
ID ADO39258 standard; protein; 285 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 921.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 285;
Best Local Similarity 25.5%; Pred. No. 0.53;
RESULT 645
ID ADO39262 standard; protein; 315 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 925.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 315;
Best Local Similarity 25.5%; Pred. No. 0.68;
RESULT 646
ID ADO39260 standard; protein; 323 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 923.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 323;
Best Local Similarity 25.5%; Pred. No. 0.7;

RESULT 647
ID ADO39261 standard; protein; 328 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 924.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 328;
Best Local Similarity 25.5%; Pred. No. 0.71;
RESULT 648
ID ADO39265 standard; protein; 338 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 928.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 338;
Best Local Similarity 25.5%; Pred. No. 0.74;
RESULT 649
ID ADO39267 standard; protein; 339 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 930.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 339;
Best Local Similarity 25.5%; Pred. No. 0.75;
RESULT 650
ID ADE28099 standard; protein; 340 AA.
DE Human NTRAN protein - SEQ ID 4.
PN W02003051902-A1.
PD 26-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 7.2%; Score 85.5; DB 7; Length 340;
Best Local Similarity 25.5%; Pred. No. 0.75;
RESULT 651
ID ADO39269 standard; protein; 384 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 932.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 384;
Best Local Similarity 25.5%; Pred. No. 0.89;
RESULT 652
ID ADO39264 standard; protein; 390 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 927.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 7.2%; Score 85.5; DB 8; Length 390;
Best Local Similarity 25.5%; Pred. No. 0.91;
RESULT 653
ID ABU26680 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #12207.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 85.5; DB 6; Length 396;
Best Local Similarity 21.0%; Pred. No. 0.93;
RESULT 654
ID AAM13575 standard; protein; 438 AA.
DE Batten disease polypeptide CLN3.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GENO-) GEN HOSPITAL CORP.
PA (UYLR-) RIKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;
Best Local Similarity 25.5%; Pred. No. 1.1;
RESULT 655
ID AAM13589 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L204.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GENO-) GEN HOSPITAL CORP.
PA (UYLR-) RIKSUNIV LEIDEN.
Query Match 7.2%; Score 85.5; DB 2; Length 438;

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Best Local Similarity 24.8%; Pred. No. 1.1;
RESULT 656
ID AAM13582 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L46.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UTLE-) RIJXSUNIV LEIDEN.
Query Match
Best Local Similarity 25.5%; Pred. No. 1.1; Length 438;
RESULT 657
ID AAM13577 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L39.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UTLE-) RIJXSUNIV LEIDEN.
Query Match
Best Local Similarity 25.5%; Pred. No. 1.1; Length 438;
RESULT 658
ID ADQ96392 standard; protein; 438 AA.
DE T cell activation associated protein #285.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 25.5%; Pred. No. 1.1; Length 438;
RESULT 659
ID ADQ39268 standard; protein; 438 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 931.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match
Best Local Similarity 25.5%; Pred. No. 1.1; Length 438;
RESULT 660
ID ADA05822 standard; protein; 440 AA.
DE Human NOV43a protein SEQ ID NO:182.
PN W02003029424-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 25.2%; Pred. No. 1.1; Length 440;
RESULT 661
ID ADN63244 standard; protein; 440 AA.
DE Human NOV43a variant.
PN U62004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILT/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEXUDA R.
PA (UTUT/) JU J.
PA (LILU/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALV/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
Query Match
Best Local Similarity 25.2%; Pred. No. 1.1; Length 440;
RESULT 662
ID ADN62985 standard; protein; 440 AA.
DE Human NOV43a.
PN U62004038223-A1.
PD 26-FEB-2004.
PA (SMIT/) SMITHSON G.
PA (MILT/) MILLET I.
PA (PEYM/) PEYMAN J A.
PA (KEKU/) KEXUDA R.
PA (UTUT/) JU J.
PA (LILU/) LI L.
PA (GUOX/) GUO X.
PA (PAT/) PATURAJAN M.
PA (SPYT/) SPYTEK K A.
PA (EDIN/) EDINGER S R.
PA (ELLE/) ELLERMAN K.
PA (MALV/) MALYANKAR U M.
PA (ORTT/) ORT T.
PA (GORM/) GORMAN L.
PA (ZERR/) ZERRHUSEN B D.
PA (ANDE/) ANDERSON D W.
PA (ZHON/) ZHONG M.
PA (CATT/) CATTERTON E.
PA (JIMW/) JI W.
PA (MILT/) MILLET I.
PA (RAST/) RASTELLI L.
PA (STON/) STONE D J.
PA (PENA/) PENA C E A.
PA (SHEN/) SHENOY S G.
PA (SHIM/) SHIMKETS R A.
PA (ROTH/) ROTHENBERG M E.
PA (LEAC/) LEACH M D.
PA (AGEE/) AGEE M L.
PA (BERG/) BERGHS C.
PA (DIP/) DIPPO V A.
PA (EISE/) EISEN A.
PA (GANG/) GANGOLLI E A.
PA (RIEG/) RIEGER D K.
PA (SPAD/) SPADERNA S K.
Query Match
Best Local Similarity 25.2%; Pred. No. 1.1; Length 440;
RESULT 663
ID AAM13593 standard; protein; 467 AA.
DE Batten disease CLN3 mutant protein in family L61.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO ) GEN HOSPITAL CORP.
PA (UTLE-) RIJXSUNIV LEIDEN.
Query Match
Best Local Similarity 25.5%; Pred. No. 1.2; Length 467;
RESULT 664
ID ABB89640 standard; protein; 473 AA.
DE Human polypeptide SEQ ID NO 2016.
PN W0200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 25.2%; Pred. No. 1.2; Length 473;
RESULT 665
ID ADQ18055 standard; protein; 473 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 872.
PN W02004048938-A2.

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PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 7.2%; Score 85.5; DB 8; Length 473;
Best Local Similarity 25.2%; Pred. No. 1.2;
RESULT 666
ID ABU40544 standard; protein; 500 AA.
DE Protein encoded by Prokaryotic essential gene #26071.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 7.2%; Score 85.5; DB 6; Length 500;
Best Local Similarity 26.0%; Pred. No. 1.3;
RESULT 667
ID ABU33210 standard; protein; 430 AA.
DE Protein encoded by Prokaryotic essential gene #18737.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 7.1%; Score 84.5; DB 6; Length 430;
Best Local Similarity 25.5%; Pred. No. 1.4;
RESULT 668
ID AAM1358 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L10.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 7.1%; Score 84.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 1.4;
RESULT 669
ID AAG16921 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17749.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 7.0%; Score 83.5; DB 3; Length 322;
Best Local Similarity 33.7%; Pred. No. 1.2;
RESULT 670
ID AAG21285 standard; protein; 472 AA.
DE Novel human diagnostic protein #21276.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 7.0%; Score 83.5; DB 4; Length 472;
Best Local Similarity 20.1%; Pred. No. 2;
RESULT 671
ID ABU35608 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #21135.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 6.9%; Score 82.5; DB 6; Length 239;
Best Local Similarity 21.7%; Pred. No. 1;
RESULT 672
ID AAM13590 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L216.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 6.9%; Score 82.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 2.4;
RESULT 673
ID ADB85263 standard; protein; 589 AA.
DE Mouse RNAI homologue SEQ ID NO:144.
PN EP1284297-A2.
PD 19-FEB-2003.
PA (WARN-) WARNER LAMBERT CO.
Query Match 6.9%; Score 82; DB 7; Length 589;
Best Local Similarity 19.5%; Pred. No. 4.2;
RESULT 674
ID AAM13586 standard; protein; 438 AA.
DE Batten disease CLN3 mutant protein in family L285.
PN W09708308-A1.

PD 06-MAR-1997.
PA (GEHO-) GEN HOSPITAL CORP.
Query Match 6.8%; Score 81.5; DB 2; Length 438;
Best Local Similarity 24.8%; Pred. No. 3.2;
RESULT 675
ID AAB92924 standard; protein; 519 AA.
DE Human protein sequence SEQ ID NO:11574.
PN EP1074617-A2.
PD 07-FEB-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.8%; Score 81.5; DB 4; Length 519;
Best Local Similarity 22.6%; Pred. No. 4;
RESULT 676
ID ADE28193 standard; protein; 577 AA.
DE Human MDR1 protein - SEQ ID 43.
PN W02003046152-A2.
PD 05-JUN-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.8%; Score 81.5; DB 7; Length 577;
Best Local Similarity 22.6%; Pred. No. 4.6;
RESULT 677
ID ADN23155 standard; protein; 529 AA.
DE Bacterial polypeptide #5808.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.8%; Score 81; DB 8; Length 529;
Best Local Similarity 23.1%; Pred. No. 4.7;
RESULT 678
ID ADN23156 standard; protein; 529 AA.
DE Bacterial polypeptide #5809.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SIAT/) SIATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.8%; Score 81; DB 8; Length 529;
Best Local Similarity 23.1%; Pred. No. 4.7;
RESULT 679
ID AAG53771 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68491.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.7;
RESULT 680
ID AAG25639 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29783.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.7;
RESULT 681
ID AAG53746 standard; protein; 322 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68457.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.7%; Score 80.5; DB 3; Length 322;
Best Local Similarity 32.7%; Pred. No. 2.7;
RESULT 682
ID ABO63194 standard; protein; 350 AA.
DE Klebsiella pneumoniae polypeptide seqid 9711.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.7%; Score 80.5; DB 7; Length 350;

Best Local Similarity 31.8%; Pred. No. 3;
RESULT 683
ID ABB48552 standard; protein; 463 AA.
DE Isteria monocytogenes protein #1256.
PN W0200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.7%; Score 80.5; DB 5; Length 463;
Best Local Similarity 19.0%; Pred. No. 4.5;
RESULT 684
ID ABB3336 standard; protein; 463 AA.
DE Protein encoded by Prokaryotic essential gene #16563.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 80.5; DB 6; Length 463;
Best Local Similarity 19.0%; Pred. No. 4.5;
RESULT 685
ID ABB43870 standard; protein; 536 AA.
DE Chlamydia trachomatis immunogenic protein, SEQ ID No 165.
PN W02003049762-A2.
PD 19-JUN-2003.
PA (CHIR-) CHIRON SPA.
Query Match 6.7%; Score 80.5; DB 7; Length 536;
Best Local Similarity 25.2%; Pred. No. 5.5;
RESULT 686
ID ABB42920 standard; protein; 891 AA.
DE Vaccinia Virus Major Core protein Paa precursor.
PN W02003017943-A2.
PD 06-MAR-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 6.7%; Score 80.5; DB 7; Length 891;
Best Local Similarity 23.3%; Pred. No. 11;
RESULT 687
ID ABB92830 standard; protein; 1780 AA.
DE Herbicidially active polypeptide SEQ ID NO 2041.
PN W0200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.7%; Score 80.5; DB 5; Length 1780;
Best Local Similarity 20.8%; Pred. No. 29;
RESULT 688
ID AAB54399 standard; protein; 144 AA.
DE Human pancreatic cancer antigen protein sequence SEQ ID NO:851.
PN W0200055320-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 3; Length 144;
Best Local Similarity 25.4%; Pred. No. 1;
RESULT 689
ID AAM39952 standard; protein; 238 AA.
DE Human polypeptide SEQ ID NO 3097.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 80; DB 4; Length 238;
Best Local Similarity 22.5%; Pred. No. 2;
RESULT 690
ID ADM04473 standard; protein; 238 AA.
DE Human protein of the invention SEQ ID NO:3158.
PN EPI347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.7%; Score 80; DB 7; Length 238;
Best Local Similarity 22.5%; Pred. No. 2;
RESULT 691
ID AAM41738 standard; protein; 249 AA.
DE Human polypeptide SEQ ID NO 6669.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.7%; Score 80; DB 4; Length 249;
Best Local Similarity 22.5%; Pred. No. 2.2;

RESULT 692
ID AAR77844 standard; protein; 309 AA.
DE Molasses toxicity resistance protein RTW1.
PN W09514774-A2.
PD 01-JUN-1995.
PA (CNRS) CENT NAT RECH SCI.
Query Match 6.7%; Score 80; DB 2; Length 309;
Best Local Similarity 28.0%; Pred. No. 2.9;
RESULT 693
ID AAB67388 standard; protein; 330 AA.
DE Photorehabdus luminescens protein sequence #485.
PN W0200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CENT NAT RECH SCI.
Query Match 6.7%; Score 80; DB 6; Length 330;
Best Local Similarity 24.6%; Pred. No. 3.2;
RESULT 694
ID AAB03831 standard; protein; 360 AA.
DE Human gene 14 encoded secreted protein HDGFN31, SEQ ID NO: 77.
PN W0200136440-A1.
PD 25-MAY-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 4; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.6;
RESULT 695
ID ABB64559 standard; protein; 360 AA.
DE Human albumin fusion protein #1234.
PN W0200177137-A1.
PD 18-OCT-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.7%; Score 80; DB 5; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.6;
RESULT 696
ID ADL77826 standard; protein; 360 AA.
DE Albumin fusion protein related therapeutic protein X, SEQ ID No 1308.
PN US2004010134-A1.
PD 15-JAN-2004.
PA (ROSE/) ROSEN C A.
PA (HASE/) HASELTINE W A.
Query Match 6.7%; Score 80; DB 8; Length 360;
Best Local Similarity 22.5%; Pred. No. 3.6;
RESULT 697
ID ABB25554 standard; protein; 365 AA.
DE Protein encoded by Prokaryotic essential gene #11081.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.7%; Score 79.5; DB 6; Length 365;
Best Local Similarity 21.2%; Pred. No. 4.2;
RESULT 698
ID AAR58703 standard; protein; 406 AA.
DE HCMV IE-exon-4 subunit.
PN W09417810-A1.
PD 18-AUG-1994.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match 6.7%; Score 79.5; DB 2; Length 406;
Best Local Similarity 19.3%; Pred. No. 4.9;
RESULT 699
ID AAM27275 standard; protein; 406 AA.
DE Human cytomagalovirus immediate-early exon 4 product.
PN W09740165-A1.
PD 30-OCT-1997.
PA (WIST-) WISTAR INST ANATOMY & BIOLOGY.
Query Match 6.7%; Score 80; DB 2; Length 406;
Best Local Similarity 19.3%; Pred. No. 4.9;
RESULT 700
ID ABB58483 standard; protein; 638 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 2241.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.7%; Score 79.5; DB 4; Length 638;

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Best Local Similarity 20.5%; Pred. No. 9.1;
RESULT 701
ID ABE13277 standard; protein; 723 AA.
DE Human transporters and ion channels (TRICH)-4.
PN W0200177174-A2.
PD 18-OCT-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 6.6%; Score 79.5; DB 5; Length 723;
Best Local Similarity 18.0%; Pred. No. 11;
RESULT 702
ID ADL12774 standard; protein; 723 AA.
DE Human steroid-induced C3A liver cell protein #80.
PN US6673549-B1.
PD 06-JAN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.7%; Score 79.5; DB 8; Length 723;
Best Local Similarity 18.0%; Pred. No. 11;
RESULT 703
ID AAW20696 standard; protein; 121 AA.
DE H. pylori secreted or periplasmic protein 05ae20220orf50.
PN W09640893-A1.
PD 19-DEC-1996.
PA (ASTR-) ASTRA AB.
Query Match 6.6%; Score 79; DB 2; Length 121;
Best Local Similarity 21.4%; Pred. No. 1;
RESULT 704
ID ABB60462 standard; protein; 323 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 8178.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.6%; Score 79; DB 4; Length 323;
Best Local Similarity 18.8%; Pred. No. 4.1;
RESULT 705
ID ABR58610 standard; protein; 1531 AA.
DE Human cancer related protein SEQ ID NO:267.
PN W02003025138-A2.
PD 27-MAR-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.6%; Score 79; DB 6; Length 1531;
Best Local Similarity 24.3%; Pred. No. 35;
RESULT 706
ID ADE31753 standard; protein; 1531 AA.
DE Human 59590 protein #SEQ ID 110.
PN W02003065984-A2.
PD 14-AUG-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.6%; Score 79; DB 7; Length 1531;
Best Local Similarity 24.3%; Pred. No. 35;
RESULT 707
ID ABU62069 standard; protein; 1597 AA.
DE Human heart alpha-kinase (HK).
PN US2002177205-A1.
PD 28-NOV-2002.
PA (RYAZ-) RYAZANOV A.
Query Match 6.6%; Score 79; DB 6; Length 1597;
Best Local Similarity 24.3%; Pred. No. 37;
RESULT 708
ID ABU62070 standard; protein; 1597 AA.
DE Mouse heart alpha-kinase (HK).
PN US2002177205-A1.
PD 28-NOV-2002.
PA (RYAZ-) RYAZANOV A.
Query Match 6.6%; Score 79; DB 6; Length 1597;
Best Local Similarity 24.3%; Pred. No. 37;
RESULT 709
ID ABO55689 standard; protein; 135 AA.
DE Human genome derived single exon protein #1923.
PN US2003194704-A1.
PD 16-OCT-2003.
PA (PENN-) PENN S G.
PA (RANK-) RANK D R.
PA (HANZ-) HANZEL D K.
Query Match 6.6%; Score 78.5; DB 8; Length 135;
Best Local Similarity 59.4%; Pred. No. 1.4;
RESULT 710
ID ADB10616 standard; protein; 228 AA.
DE Altolococcus ocellus antigenic protein SEQ ID NO:4244.
PN W02003048304-A2.
PD 12-JUN-2003.
PA (AMHP-) MYETH HOLDINGS CORP.
Query Match 6.6%; Score 78.5; DB 6; Length 228;
Best Local Similarity 22.5%; Pred. No. 2.9;
RESULT 711
ID ABU36298 standard; protein; 239 AA.
DE Protein encoded by Prokaryotic essential gene #21825.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.6%; Score 78.5; DB 6; Length 239;
Best Local Similarity 23.4%; Pred. No. 3.1;
RESULT 712
ID ADJ27174 standard; protein; 626 AA.
DE Human TRICH-6, SEQ ID 6.
PN W02004013293-A2.
PD 12-FEB-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 626;
Best Local Similarity 18.0%; Pred. No. 12;
RESULT 713
ID ABW84679 standard; protein; 648 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5126.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 648;
Best Local Similarity 18.0%; Pred. No. 12;
RESULT 714
ID APW84677 standard; protein; 668 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5126.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.6%; Score 78.5; DB 8; Length 668;
Best Local Similarity 18.0%; Pred. No. 13;
RESULT 715
ID ABP29904 standard; protein; 669 AA.
DE Streptococcus polypeptide SEQ ID NO 8984.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.6%; Score 78.5; DB 5; Length 669;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 716
ID ABP28724 standard; protein; 669 AA.
DE Streptococcus polypeptide SEQ ID NO 6624.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.6%; Score 78.5; DB 5; Length 669;
Best Local Similarity 23.5%; Pred. No. 13;
RESULT 717
ID ADI21047 standard; protein; 703 AA.
DE Novel human protein #22.
PN W02003025148-A2.
PD 27-MAR-2003.
PA (HYSE-) HYSE INC.
Query Match 6.6%; Score 78.5; DB 7; Length 703;
Best Local Similarity 18.0%; Pred. No. 14;
RESULT 718
ID ABW84682 standard; protein; 711 AA.
DE Human diagnostic and therapeutic pproteins SEQ ID NO:5131.
PN W02004023973-A2.
PD 25-MAR-2004.

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PA (INCY-) INCYTE CORP.
 Query Match 6.6%; Score 78.5; DB 8; Length 711;
 Best Local Similarity 18.0%; Pred. No. 14;
 RESULT 719
 ID ABB52105 standard; protein; 723 AA.
 DE Homo sapiens ABC transporter ABCB9 protein SEQ ID NO:57.
 PN EP1217066-A1.
 PD 26-JUN-2002.
 PA (UYGE-) UNIV GENT.
 Query Match 6.6%; Score 78.5; DB 5; Length 723;
 Best Local Similarity 18.0%; Pred. No. 14;
 RESULT 720
 ID ADO97094 standard; protein; 723 AA.
 DE Human cancer associated sequence Hpl-10-005, SEQ ID 70.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 6.6%; Score 78.5; DB 8; Length 723;
 Best Local Similarity 18.0%; Pred. No. 14;
 RESULT 721
 ID AAB02437 standard; protein; 766 AA.
 DE Human ATP binding cassette, ABCB9 transporter protein.
 PN WO200140305-A1.
 PD 07-JUN-2001.
 PA (ACT1-) ACTIVE PASS PHARM INC.
 Query Match 6.6%; Score 78.5; DB 4; Length 766;
 Best Local Similarity 18.0%; Pred. No. 15;
 RESULT 722
 ID AAB02441 standard; protein; 766 AA.
 DE Human ATP binding cassette, ABCB9 transporter protein mutant K545R.
 PN WO200140305-A1.
 PD 07-JUN-2001.
 PA (ACT1-) ACTIVE PASS PHARM INC.
 Query Match 6.6%; Score 78.5; DB 4; Length 766;
 Best Local Similarity 18.0%; Pred. No. 15;
 RESULT 723
 ID AAB02442 standard; protein; 766 AA.
 DE Human ATP binding cassette, ABCB9 transporter protein mutant D667N.
 PN WO200140305-A1.
 PD 07-JUN-2001.
 PA (ACT1-) ACTIVE PASS PHARM INC.
 Query Match 6.6%; Score 78.5; DB 4; Length 766;
 Best Local Similarity 18.0%; Pred. No. 15;
 RESULT 724
 ID AAG67163 standard; protein; 766 AA.
 DE Amino acid sequence of a human 33894 transporter polypeptide.
 PN WO200164875-A2.
 PD 07-SEP-2001.
 PA (MILL-) MILLENNIUM PHARM INC.
 Query Match 6.6%; Score 78.5; DB 4; Length 766;
 Best Local Similarity 18.0%; Pred. No. 15;
 RESULT 725
 ID AAG79246 standard; protein; 766 AA.
 DE Amino acid sequence of a human TAP-like (HUTAPL) polypeptide.
 PN WO200173018-A2.
 PD 04-OCT-2001.
 PA (MERE-) MERCK PATENT GMBH.
 Query Match 6.6%; Score 78.5; DB 4; Length 766;
 Best Local Similarity 18.0%; Pred. No. 15;
 RESULT 726
 ID ABB98345 standard; protein; 766 AA.
 DE Human ABC transporter ABCB9 SEQ ID NO 6.
 PN WO200264781-A2.
 PD 22-AUG-2002.
 PA (ACT1-) ACTIVE PASS PHARM INC.
 Query Match 6.6%; Score 78.5; DB 5; Length 766;
 Best Local Similarity 18.0%; Pred. No. 15;
 RESULT 727
 ID AAE21170 standard; protein; 766 AA.
 DE Human TRICH-14 protein.
 PN WO200212340-A2.
 PD 14-FEB-2002.
 PA (INCY-) INCYTE GENOMICS INC.

Query Match 6.6%; Score 78.5; DB 5; Length 766;
 Best Local Similarity 18.0%; Pred. No. 15;
 RESULT 728
 ID ADO97096 standard; protein; 766 AA.
 DE Human cancer associated sequence HP2-10-005, SEQ ID 72.
 PN WO2004060304-A2.
 PD 22-JUL-2004.
 PA (SAGR-) SAGRES DISCOVERY INC.
 Query Match 6.6%; Score 78.5; DB 8; Length 766;
 Best Local Similarity 18.0%; Pred. No. 15;
 RESULT 729
 ID AAG20805 standard; protein; 377 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 23131.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.5%; Score 78; DB 3; Length 377;
 Best Local Similarity 23.8%; Pred. No. 6.6;
 RESULT 730
 ID AAG20804 standard; protein; 442 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 23130.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.5%; Score 78; DB 3; Length 442;
 Best Local Similarity 23.8%; Pred. No. 8.2;
 RESULT 731
 ID AAU35545 standard; protein; 471 AA.
 DE Haemophilus influenzae cellular proliferation protein #186.
 PN WO200170955-A2.
 PD 27-SEP-2001.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.5%; Score 78; DB 4; Length 471;
 Best Local Similarity 25.0%; Pred. No. 9;
 RESULT 732
 ID ABU30411 standard; protein; 471 AA.
 DE Protein encoded by Prokaryotic essential gene #15938.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 6.5%; Score 78; DB 6; Length 471;
 Best Local Similarity 25.0%; Pred. No. 9;
 RESULT 733
 ID AAG20803 standard; protein; 489 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 23129.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.5%; Score 78; DB 3; Length 489;
 Best Local Similarity 23.8%; Pred. No. 9.5;
 RESULT 734
 ID ABB49039 standard; protein; 269 AA.
 DE Listeria monocytogenes protein #1743.
 PN WO200177335-A2.
 PD 18-OCT-2001.
 PA (INSP) INST PASTEUR.
 Query Match 6.5%; Score 77.5; DB 5; Length 269;
 Best Local Similarity 22.0%; Pred. No. 4.7;
 RESULT 735
 ID ABG17374 standard; protein; 280 AA.
 DE Novel human diagnostic protein #17365.
 PN WO200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.5%; Score 77.5; DB 4; Length 280;
 Best Local Similarity 21.9%; Pred. No. 5;
 RESULT 736
 ID ABO00771 standard; protein; 280 AA.
 DE Polypeptide encoded by novel human contig #22.
 PN WO2003023013-A2.
 PD 20-MAR-2003.
 PA (HYSE-) HYSEQ INC.
 Query Match 6.5%; Score 77.5; DB 6; Length 280;
 Best Local Similarity 21.9%; Pred. No. 5;
 RESULT 737
 ID ABU4889 standard; protein; 327 AA.

DE Protein encoded by Prokaryotic essential gene #34416.
PN W0200277183-A2.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 77.5; DB 6; Length 327;
Best Local Similarity 24.8%; Pred. No. 6.2;
RESULT 738
ID AAM13576 standard; protein: 438 AA.
DE Mouse Batten disease polypeptide C1N3 homologue.
PN W09708308-A1.
PD 06-MAR-1997.
PA (GEHO) GEN HOSPITAL CORP.
PA (UYLR-) RIJXSUNIV LEIDEN.
Query Match 6.5%; Score 77.5; DB 2; Length 438;
Best Local Similarity 27.6%; Pred. No. 9.3;
RESULT 739
ID ADS42965 standard; protein: 491 AA.
DE Bacterial polypeptide #21395.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOV-) CAO Y.
PA (HINK-) HINKLE G J.
PA (SLAT-) SLATER S C.
PA (CHEN-) CHEN X.
PA (GOLD-) GOLDMAN B S.
Query Match 6.5%; Score 77.5; DB 8; Length 491;
Best Local Similarity 22.6%; Pred. No. 11;
RESULT 740
ID ADC42919 standard; protein: 892 AA.
DE Variola smallpox virus A10L.
PN W02003017943-A2.
PD 06-MAR-2003.
PA (MYRI-) MYRIAD GENETICS INC.
Query Match 6.5%; Score 77.5; DB 7; Length 892;
Best Local Similarity 22.7%; Pred. No. 25;
RESULT 741
ID AAR88413 standard; protein: 353 AA.
DE High-affinity melatonin-1a receptor.
PN W09535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.9;
RESULT 742
ID AAM23958 standard; protein: 353 AA.
DE Mouse melatonin 1a receptor.
PN W09803549-A1.
PD 29-JAN-1998.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 77; DB 2; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.9;
RESULT 743
ID ABB07571 standard; protein: 353 AA.
DE Mouse melatonin 1a (Mella) receptor.
PN US6326526-B1.
PD 04-DEC-2001.
PA (BRIM-) BRISTOL-MYERS SQUIBB CO.
PA (GEHO) GEN HOSPITAL CORP.
Query Match 6.4%; Score 77; DB 5; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.9;
RESULT 744
ID ADO29553 standard; protein: 353 AA.
DE Mouse GPCR MTR1A, SEQ ID NO:655.
PN W02004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.4%; Score 77; DB 8; Length 353;
Best Local Similarity 22.1%; Pred. No. 7.9;
RESULT 745
ID ADM25403 standard; protein: 383 AA.
DE Hyperthermophile Mechanopyrus kandleri protein #9.
PN W02003076575-A2.
PD 18-SEP-2003.

PA (FIDE-) FIDELITY SYSTEMS INC.
PA (MALY-) MALYKH A.
Query Match 6.4%; Score 77; DB 7; Length 383;
Best Local Similarity 24.8%; Pred. No. 8.9;
RESULT 746
ID ADO95948 standard; protein: 490 AA.
DE T cell activation associated protein #63.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.4%; Score 77; DB 8; Length 490;
Best Local Similarity 19.5%; Pred. No. 12;
RESULT 747
ID ADO96002 standard; protein: 490 AA.
DE T cell activation associated protein #90.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.4%; Score 77; DB 8; Length 490;
Best Local Similarity 19.5%; Pred. No. 12;
RESULT 748
ID AAG42521 standard; protein: 648 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53040.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 648;
Best Local Similarity 20.4%; Pred. No. 18;
RESULT 749
ID ABU16172 standard; protein: 650 AA.
DE Protein encoded by Prokaryotic essential gene #1699.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.4%; Score 77; DB 6; Length 650;
Best Local Similarity 27.5%; Pred. No. 18;
RESULT 750
ID ABW2713 standard; protein: 650 AA.
DE Staphylococcus aureus protein #1953.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.4%; Score 77; DB 6; Length 650;
Best Local Similarity 27.5%; Pred. No. 18;
RESULT 751
ID AAG42520 standard; protein: 690 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53039.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 690;
Best Local Similarity 20.4%; Pred. No. 20;
RESULT 752
ID AAG42519 standard; protein: 728 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 53038.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 728;
Best Local Similarity 20.4%; Pred. No. 22;
RESULT 753
ID AAG32549 standard; protein: 805 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39287.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 805;
Best Local Similarity 20.4%; Pred. No. 25;
RESULT 754
ID AAG32548 standard; protein: 847 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39286.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.4%; Score 77; DB 3; Length 847;
Best Local Similarity 20.4%; Pred. No. 27;
RESULT 755
ID AAG32547 standard; protein: 991 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 39285.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 77; DB 3; Length 991;
RESULT 756
ID ABP52133 standard; protein; 1025 AA.
DE Plasmodium falciparum multidrug resistance protein SEQ ID NO: 85.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match
Best Local Similarity 6.4%; Score 77; DB 5; Length 1025;
RESULT 757
ID AAG42381 standard; protein; 1047 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52849.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 77; DB 3; Length 1047;
RESULT 758
ID AAG42380 standard; protein; 1191 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52848.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 77; DB 3; Length 1191;
RESULT 759
ID AAG42379 standard; protein; 1202 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52847.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 6.4%; Score 77; DB 3; Length 1202;
RESULT 760
ID AAR29527 standard; protein; 2510 AA.
DE HCV antigen T7N1-30.
PN EP51813-A2.
PD 16-DEC-1992.
PA (MITU) MITSUBISHI KASEI CORP.
Query Match
Best Local Similarity 6.4%; Score 77; DB 2; Length 2510;
RESULT 761
ID ADF74966 standard; protein; 249 AA.
DE Human 164-1h protein (SeqID 25).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 8; Length 249;
RESULT 762
ID ADC01137 standard; protein; 278 AA.
DE Enterohaemorrhagic E. coli O157:H7-specific protein SEQ ID NO: 1181.
PN JP2002355074-A.
PD 10-DEC-2002.
PA (UYTS-) UNIV TSUKUBA.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 7; Length 278;
RESULT 763
ID ABO65627 standard; protein; 435 AA.
DE Klebsiella pneumoniae polypeptide Seqid 12344.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 7; Length 435;
RESULT 764
ID ADF74969 standard; protein; 481 AA.
DE Human 164-1b protein (SeqID 28).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 8; Length 481;

Best Local Similarity 23.3%; Pred. No. 14;
RESULT 765
ID AAR90765 standard; protein; 494 AA.
DE Human K+ channel 2 mature protein.
PN WO9603415-A1.
PD 08-FEB-1996.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 2; Length 494;
RESULT 766
ID AAM42996 standard; protein; 494 AA.
DE Putative mature potassium channel 2 protein.
PN US5710019-A.
PD 20-JAN-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 2; Length 494;
RESULT 767
ID ABP58356 standard; protein; 494 AA.
DE Human potassium channel subunit Kv5.1.
PN WO200296944-A2.
PD 05-DEC-2002.
PA (VLA-) VLAAMS INTERUNIVERSITAIR INST BIOTECHNOG.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 6; Length 494;
RESULT 768
ID ADC99155 standard; protein; 494 AA.
DE Human mature K+ channel 2 protein.
PN US2003092895-A1.
PD 15-MAY-2003.
PA (LITY/) LI Y.
PA (ADAM/) ADAMS M D.
PA (WHIT/) WHITE O R.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 7; Length 494;
RESULT 769
ID AAW20085 standard; protein; 509 AA.
DE Helicobacter pylori cytoplasmic protein, 10009666.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR-) ASTRA AB.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 2; Length 509;
RESULT 770
ID ADQ07984 standard; protein; 526 AA.
DE Human hypothetical protein FLJ20371-encoding cDNA.
PN WO2004061123-A2.
PD 22-JUL-2004.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 8; Length 526;
RESULT 771
ID ADP25065 standard; protein; 526 AA.
DE PRO polypeptide SEQ ID NO: 2243.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GENT-) GENENTECH INC.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 8; Length 526;
RESULT 772
ID ADB63857 standard; protein; 555 AA.
DE Human protein encoded by clone ASTRO20053430.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELT-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match
Best Local Similarity 6.4%; Score 76.5; DB 7; Length 555;
RESULT 773
ID ABB08159 standard; protein; 570 AA.
DE Human cytoskeleton-associated protein (CSAP)-3 (ID: 7091536CD1).
PN WO200242330-A2.
PD 30-MAY-2002.

PA (INCY-) INCYTE GENOMICS INC.
 Query Match 6.4%; Score 76.5; DB 5; Length 570;
 Best Local Similarity 23.3%; Pred. No. 18;
 RESULT 774
 ID AAM20918 standard; protein; 593 AA.
 DE H. pylori transporter protein, 149p12015orf14.
 PN M09640893-A1.
 PD 19-DEC-1996.
 PA (ASTR) ASTRA AB.
 Query Match 6.4%; Score 76.5; DB 2; Length 593;
 Best Local Similarity 19.2%; Pred. No. 19;
 RESULT 775
 ID ADN46225 standard; protein; 615 AA.
 DE Thermococcus kodakaraensis KOD1 protein sequence SeqID103.
 PN M02004022736-A1.
 PD 18-MAR-2004.
 PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
 Query Match 6.4%; Score 76.5; DB 8; Length 615;
 Best Local Similarity 22.6%; Pred. No. 20;
 RESULT 776
 ID ADN21126 standard; protein; 2539 AA.
 DE Bacterial polypeptide #3779.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 6.4%; Score 76.5; DB 8; Length 2539;
 Best Local Similarity 22.1%; Pred. No. 1.4e+02;
 RESULT 777
 ID ADH88107 standard; protein; 195 AA.
 DE Enterococcus faecalis polypeptide #2587.
 PN US6617156-B1.
 PD 09-SEP-2003.
 PA (DOUC/) DOUCETTE-STAMM L A.
 PA (BUSH/) BUSH D.
 Query Match 6.4%; Score 76; DB 7; Length 195;
 Best Local Similarity 25.9%; Pred. No. 4.6;
 RESULT 778
 ID AAG09592 standard; protein; 274 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 7586.
 PN EF1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.4%; Score 76; DB 3; Length 274;
 Best Local Similarity 26.7%; Pred. No. 7.3;
 RESULT 779
 ID AAG09591 standard; protein; 287 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 7585.
 PN EF1033405-A2.
 PD 06-SEP-2000.
 Query Match 6.4%; Score 76; DB 3; Length 287;
 Best Local Similarity 26.7%; Pred. No. 7.8;
 RESULT 780
 ID ADQ96244 standard; protein; 366 AA.
 DE T cell activation associated protein #211.
 PN M02004058805-A2.
 PD 15-JUL-2004.
 PA (ASAH-) ASAH KASEI PHARMA CORP.
 Query Match 6.4%; Score 76; DB 8; Length 366;
 Best Local Similarity 22.0%; Pred. No. 11;
 RESULT 781
 ID ADQ96246 standard; protein; 366 AA.
 DE T cell activation associated protein #212.
 PN M02004058805-A2.
 PD 15-JUL-2004.
 PA (ASAH-) ASAH KASEI PHARMA CORP.
 Query Match 6.4%; Score 76; DB 8; Length 366;
 Best Local Similarity 22.0%; Pred. No. 11;
 RESULT 782
 ID ABB89424 standard; protein; 456 AA.
 DE Human polypeptide SEQ ID NO 1800.

PN M0200190304-A2.
 PD 28-NOV-2001.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.4%; Score 76; DB 5; Length 456;
 Best Local Similarity 22.0%; Pred. No. 15;
 RESULT 783
 ID AAB53400 standard; protein; 557 AA.
 DE Human colon cancer antigen protein sequence SEQ ID NO:940.
 PN M0200055351-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 6.4%; Score 76; DB 3; Length 557;
 Best Local Similarity 22.0%; Pred. No. 20;
 RESULT 784
 ID AAY44945 standard; protein; 593 AA.
 DE Wheat sulphate permease-2.
 PN M0200004154-A2.
 PD 27-JAN-2000.
 PA (DUPO) DU PONT DE NEMOURS & CO E I.
 Query Match 6.4%; Score 76; DB 3; Length 593;
 Best Local Similarity 21.4%; Pred. No. 21;
 RESULT 785
 ID ADN22849 standard; protein; 1402 AA.
 DE Bacterial polypeptide #5502.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 6.4%; Score 76; DB 8; Length 1402;
 Best Local Similarity 20.2%; Pred. No. 70;
 RESULT 786
 ID ADN23383 standard; protein; 1917 AA.
 DE Bacterial polypeptide #6036.
 PN US2003233675-A1.
 PD 18-DEC-2003.
 PA (CAOY/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match 6.4%; Score 76; DB 8; Length 1917;
 Best Local Similarity 18.5%; Pred. No. 1.1e+02;
 RESULT 787
 ID AAB63150 standard; protein; 228 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 16242.
 PN M0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 6.3%; Score 75.5; DB 4; Length 228;
 Best Local Similarity 21.8%; Pred. No. 6.5;
 RESULT 788
 ID ADK46633 standard; protein; 263 AA.
 DE Streptococcus pneumoniae protein, Seq ID No 3148.
 PN US6699703-B1.
 PD 02-MAR-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 6.3%; Score 75.5; DB 8; Length 263;
 Best Local Similarity 18.0%; Pred. No. 7.9;
 RESULT 789
 ID ADM92206 standard; protein; 263 AA.
 DE S pneumoniae antigenic protein sequence SeqID403.
 PN M02004020609-A2.
 PD 11-MAR-2004.
 PA (TUFT) UNIV TUFTS.
 Query Match 6.3%; Score 75.5; DB 8; Length 263;
 Best Local Similarity 18.0%; Pred. No. 7.9;
 RESULT 790
 ID AAY81619 standard; protein; 264 AA.
 DE Streptococcus pneumoniae type 4 protein sequence #119.
 PN M0200006737-A2.

PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNICS LTD.
Query Match 6.3%; Score 75.5; DB 3; Length 264;
Best Local Similarity 18.0%; Pred. No. 7.9;
RESULT 791
ID ADR96242 standard; protein; 264 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 4877.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 75.5; DB 8; Length 264;
Best Local Similarity 18.0%; Pred. No. 7.9;
RESULT 792
ID AEU02182 standard; protein; 276 AA.
DE S. pneumoniae type 4 strain protein from coding region #1759.
PN W0200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.3%; Score 75.5; DB 6; Length 276;
Best Local Similarity 18.0%; Pred. No. 8.4;
RESULT 793
ID AAG93285 standard; protein; 342 AA.
DE C. albicans BAX-associated protein fragment SEQ ID 528.
PN W0200264766-A2.
PD 22-AUG-2002.
PA (JANC) JANSSEN PHARM NV.
Query Match 6.3%; Score 75.5; DB 5; Length 342;
Best Local Similarity 21.9%; Pred. No. 11;
RESULT 794
ID AAB15936 standard; protein; 352 AA.
DE E. coli proliferation associated protein sequence SEQ ID NO:293.
PN W0200044906-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.3%; Score 75.5; DB 3; Length 352;
Best Local Similarity 31.7%; Pred. No. 12;
RESULT 795
ID ADH51470 standard; protein; 363 AA.
DE Rat M1 receptor amino acid sequence #SEQ ID 2.
PN PR2835847-A1.
PD 15-AUG-2003.
PA (SERV-) LES LAB SERVIER SA.
Query Match 6.3%; Score 75.5; DB 7; Length 363;
Best Local Similarity 23.5%; Pred. No. 12;
RESULT 796
ID AAU03851 standard; protein; 397 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #23.
PN W0200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 397;
Best Local Similarity 19.1%; Pred. No. 14;
RESULT 797
ID AAU03852 standard; protein; 433 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #24.
PN W0200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 433;
Best Local Similarity 19.1%; Pred. No. 16;
RESULT 798
ID ADS24239 standard; protein; 463 AA.
DE Bacterial polypeptide #13272.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 6.3%; Score 75.5; DB 8; Length 463;
Best Local Similarity 21.4%; Pred. No. 17;
RESULT 799
ID ADO29507 standard; protein; 471 AA.
DE Mouse GPCR HTR2A, SEQ ID NO:609.
PN W0200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMM INC.
Query Match 6.3%; Score 75.5; DB 8; Length 471;
Best Local Similarity 21.0%; Pred. No. 18;
RESULT 800
ID AAU03820 standard; protein; 499 AA.
DE G protein-coupled receptor-like (GPCR-like) receptor protein #19.
PN W0200138533-A2.
PD 31-MAY-2001.
PA (PHAA) PHARMACIA & UPJOHN.
Query Match 6.3%; Score 75.5; DB 4; Length 499;
Best Local Similarity 19.1%; Pred. No. 19;
RESULT 801
ID ADM72132 standard; protein; 392 AA.
DE Human NTRAN polypeptide (clone ID 752455CD1).
PN W02004022705-A2.
PD 18-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.3%; Score 75; DB 8; Length 392;
Best Local Similarity 21.0%; Pred. No. 16;
RESULT 802
ID AAU45917 standard; protein; 445 AA.
DE Propionibacterium acnes immunogenic protein #6813.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 75; DB 4; Length 445;
Best Local Similarity 24.8%; Pred. No. 19;
RESULT 803
ID ABW42436 standard; protein; 445 AA.
DE Propionibacterium acnes predicted ORF-encoded polypeptide #7112.
PN W02003033515-A1.
PD 24-APR-2003.
PA (CORI-) CORIXA CORP.
Query Match 6.3%; Score 75; DB 6; Length 445;
Best Local Similarity 24.8%; Pred. No. 19;
RESULT 804
ID ADA34178 standard; protein; 467 AA.
DE Actinobacter Daumannli protein #1339.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.3%; Score 75; DB 6; Length 467;
Best Local Similarity 23.1%; Pred. No. 20;
RESULT 805
ID ADR14597 standard; protein; 473 AA.
DE Human NF-kappaB pathway-associated protein SeqID598.
PN W02004065577-A2.
PD 05-AUG-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 6.3%; Score 75; DB 8; Length 473;
Best Local Similarity 21.0%; Pred. No. 20;
RESULT 806
ID ADP99138 standard; protein; 480 AA.
DE Human transporter and ion channel (TRICH) protein - SEQ ID 3.
PN W02004048599-A2.
PD 10-JUN-2004.
PA (INCY-) INCYTE CORP.
Query Match 6.3%; Score 75; DB 8; Length 480;
Best Local Similarity 21.0%; Pred. No. 21;
RESULT 807
ID ADH86490 standard; protein; 549 AA.
DE Enterococcus faecalis polypeptide #970.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC) DOUCETTE-STAMM L A.
PA (BUSH) BUSH D.
Query Match 6.3%; Score 75; DB 7; Length 549;
Best Local Similarity 18.7%; Pred. No. 25;

RESULT 808
ID AAB54066 standard; protein; 1051 AA.
DE Non-A, non-B hepatitis virus gene #4 product.
PN UP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYO IGAKU SOGO KENKYUSHO.
PA (SANN) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU) TONEN CORP.
Query Match 6.3%; Score 75; DB 2; Length 1051;
Best Local Similarity 23.4%; Pred. No. 62;
RESULT 809
ID AAR98361 standard; protein; 1051 AA.
DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#4).
PN JP07133291-A.
PD 23-MAY-1995.
PA (TOFU) TONEN CORP.
Query Match 6.3%; Score 75; DB 2; Length 1051;
Best Local Similarity 23.4%; Pred. No. 62;
RESULT 810
ID ADB64712 standard; protein; 1131 AA.
DE Human protein encoded by clone NT2NE20077270.
PN EPI308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.3%; Score 75; DB 7; Length 1131;
Best Local Similarity 23.9%; Pred. No. 68;
RESULT 811
ID AAB64494 standard; protein; 2248 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 20274.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.3%; Score 75; DB 4; Length 2248;
Best Local Similarity 22.9%; Pred. No. 1.8e+02;
RESULT 812
ID ADG20763 standard; protein; 2248 AA.
DE Drosophila melanogaster rutabaga protein SEQ ID NO:2.
PN WO2003103704-A2.
PD 18-DEC-2003.
PA (DEVE-) DEVELOPMENTAL BIOLOGISCHE FORSCH.
Query Match 6.3%; Score 75; DB 8; Length 2248;
Best Local Similarity 22.9%; Pred. No. 1.8e+02;
RESULT 813
ID AQQ89656 standard; protein; 2248 AA.
DE Antagonist of cell cycle progression polypeptide #43.
PN WO2004063362-A2.
PD 29-JUL-2004.
PA (CYCL-) CYCLACEL LTD.
Query Match 6.3%; Score 75; DB 8; Length 2248;
Best Local Similarity 22.9%; Pred. No. 1.8e+02;
RESULT 814
ID AAB66797 standard; protein; 200 AA.
DE Porcine reproductive and respiratory syndrome virus ORF #5 protein.
PN WO200102858-A1.
PD 11-JAN-2001.
PA (MOLE-) INST MOLECULAR AGROBIOLOGY.
PA (MATE-) INST MATERIALS RES & ENG.
Query Match 6.2%; Score 74.5; DB 4; Length 200;
Best Local Similarity 23.8%; Pred. No. 7.1;
RESULT 815
ID ADP74954 standard; protein; 256 AA.
DE Rat 164-1h protein (SeqID 13).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEEDA CHEM IND LTD.
Query Match 6.2%; Score 74.5; DB 8; Length 256;
Best Local Similarity 23.3%; Pred. No. 10;
RESULT 816
ID AAR53748 standard; protein; 355 AA.
DE Seven transmembrane receptor (V28).
PN WO9412635-A2.
PD 09-JUN-1994.

PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 2; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 817
ID AAW48722 standard; protein; 355 AA.
DE Human V28 seven transmembrane receptor.
PN US5759804-A.
PD 02-JUN-1998.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 2; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 818
ID AAY90677 standard; protein; 355 AA.
DE Human mutant G protein-coupled receptor V28 (I230K).
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 819
ID AAY90642 standard; protein; 355 AA.
DE Human G protein-coupled receptor V28.
PN WO200022129-A1.
PD 20-APR-2000.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 820
ID AAB21693 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #2.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 821
ID AAB21692 standard; protein; 355 AA.
DE Human 7TM receptor V28 cDNA clone protein #1.
PN US6107475-A.
PD 22-AUG-2000.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 822
ID AAG80126 standard; protein; 355 AA.
DE Human CX3CR1 protein.
PN WO200172830-A2.
PD 04-OCT-2001.
PA (IFP-) IPF PHARM GMBH.
PA (FORS-) FORSMANN U.
Query Match 6.2%; Score 74.5; DB 3; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 823
ID AAB82786 standard; protein; 355 AA.
DE Human CX3C chemokine receptor 1.
PN WO200160406-A1.
PD 23-AUG-2001.
PA (MILL-) MILLENNIUM PHARM INC.
PA (NOUN) UNIV NORTHWESTERN.
Query Match 6.2%; Score 74.5; DB 4; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 824
ID AAU91235 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #2.
PN US6348574-B1.
PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 825
ID AAU91234 standard; protein; 355 AA.
DE Human 7 transmembrane domain receptor V28 #1.
PN US6348574-B1.

PD 19-FEB-2002.
PA (ICOS-) ICOS CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 826
ID AAV84327 standard; protein; 355 AA.
DE Protein CX3CR1 differentially expressed in breast cancer tissue.
PN WO200210436-A2.
PD 07-FEB-2002.
PA (BGHM-) BRIGHAM & WOMENS HOSPITAL INC.
PA (BAAK/) BAAK J.
Query Match 6.2%; Score 74.5; DB 5; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 827
ID ABR58524 standard; protein; 355 AA.
DE Human chemokine (C-X3-C) receptor 1 protein.
PN WO2003025138-A2.
PD 27-MAR-2003.
PA (BOSB-) BOS BIOTECHNOLOGY INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 828
ID AAO29513 standard; protein; 355 AA.
DE Human fractalkine receptor (313) protein.
PN WO2003039475-A2.
PD 15-MAY-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 829
ID ABP97732 standard; protein; 355 AA.
DE Amino acid sequence of human chemokine receptor CX3CR1.
PN WO2003014153-A2.
PD 20-FEB-2003.
PA (TOPI-) TOPICEN PHARM INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 830
ID ABP81882 standard; protein; 355 AA.
DE Human CX3C chemokine fractalkine receptor 1 protein SEQ ID NO:249.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.2%; Score 74.5; DB 6; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 831
ID ADC22751 standard; protein; 355 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #74.
PN US655339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 832
ID ADC22649 standard; protein; 355 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #34.
PN US655339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 833
ID ADH14224 standard; protein; 355 AA.
DE Mutated human serotonin V28.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAM/) LIAM C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 834
ID ADH14122 standard; protein; 355 AA.

DE Human serotonin V28.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAM/) LIAM C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 6.2%; Score 74.5; DB 7; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 835
ID ADH10680 standard; protein; 355 AA.
DE Human CX3CR1 polypeptide.
PN WO2003104484-A1.
PD 18-DEC-2003.
PA (META-) METAPOLEX INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 836
ID ADO29269 standard; protein; 355 AA.
DE Human GPCR CX3CR1, SEQ ID NO:370.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMML INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 837
ID ADQ18141 standard; protein; 355 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 958.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 838
ID ADP56020 standard; protein; 355 AA.
DE Human PRO protein sequence SEQ ID NO:1996.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 839
ID ADP54585 standard; protein; 355 AA.
DE Human PRO protein sequence SEQ ID NO:561.
PN WO2004039956-A2.
PD 13-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 840
ID ADP23931 standard; protein; 355 AA.
DE PRO polypeptide SEQ ID NO:1109.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 841
ID ADQ39421 standard; protein; 355 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1084.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.2%; Score 74.5; DB 8; Length 355;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 842
ID ADO39422 standard; protein; 362 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1085.
PN WO2004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.2%; Score 74.5; DB 8; Length 362;
Best Local Similarity 25.8%; Pred. No. 16;
RESULT 843

ID AAM7109 standard; protein; 471 AA.
DE Rat 5-HT2A serotonin receptor C322K mutant.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 844
ID AAM7111 standard; protein; 471 AA.
DE Rat 5-HT2A serotonin receptor C322E mutant.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 845
ID AAM7110 standard; protein; 471 AA.
DE Rat 5-HT2A serotonin receptor C322R mutant.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 846
ID AAM7104 standard; protein; 471 AA.
DE Rat 5-HT2A serotonin receptor.
PN WO9838217-A1.
PD 03-SEP-1998.
PA (TEIT/) TEITLER M.
PA (HERR/) HERRICK-DAVIS K.
PA (EGAN/) EGAN C C.
Query Match 6.2%; Score 74.5; DB 2; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 847
ID AAB07980 standard; protein; 471 AA.
DE Rat 5-HT2 receptor sequence.
PN US6383762-B1.
PD 07-MAY-2002.
PA (SYNA-) SYNAPTC PHARM CORP.
Query Match 6.2%; Score 74.5; DB 5; Length 471;
Best Local Similarity 21.0%; Pred. No. 23;
RESULT 848
ID ADF74971 standard; protein; 481 AA.
DE Rat 164-1b protein (SeqID 30).
PN WO2003097686-A1.
PD 27-NOV-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.2%; Score 74.5; DB 8; Length 481;
Best Local Similarity 23.3%; Pred. No. 24;
RESULT 849
ID AAM93692 standard; protein; 562 AA.
DE Human polypeptide, SEQ ID NO: 3602.
PN EP130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INSTR.
Query Match 6.2%; Score 74.5; DB 4; Length 562;
Best Local Similarity 23.1%; Pred. No. 30;
RESULT 850
ID ADL31569 standard; protein; 562 AA.
DE Human protein encoded by a full length CDNA clone SeqID 3602.
PN EP1396543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.2%; Score 74.5; DB 8; Length 562;
Best Local Similarity 23.1%; Pred. No. 30;
RESULT 851
ID ADQ96138 standard; protein; 562 AA.
DE T cell activation associated protein #158.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 6.2%; Score 74.5; DB 8; Length 562;
Best Local Similarity 23.1%; Pred. No. 30;
RESULT 852
ID ADR86160 standard; protein; 587 AA.
DE Aspergillus fumigatus essential gene protein #210.
PN WO2004067709-A2.
PD 12-AUG-2004.
PA (ELIT-) ELITRA PHARM INC.
PA (ELIT-) ELITRA CANADA LTD.
Query Match 6.2%; Score 74.5; DB 8; Length 587;
Best Local Similarity 18.2%; Pred. No. 32;
RESULT 853
ID ABB62948 standard; protein; 597 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15636.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 6.2%; Score 74.5; DB 4; Length 597;
Best Local Similarity 27.2%; Pred. No. 32;
RESULT 854
ID ADA36878 standard; protein; 940 AA.
DE Acinetobacter baumannii protein #4039.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 74.5; DB 6; Length 940;
Best Local Similarity 21.1%; Pred. No. 61;
RESULT 855
ID ABB92731 standard; protein; 1808 AA.
DE Herbicidally active polypeptide SEQ ID NO 1942.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 6.2%; Score 74.5; DB 5; Length 1808;
Best Local Similarity 17.3%; Pred. No. 1.5e+02;
RESULT 856
ID AAE20477 standard; protein; 3010 AA.
DE HCV-S1 full-length polypeptide.
PN WO200208447-A2.
PD 31-JAN-2002.
PA (MOLE-) INST MOLECULAR & CELL BIOLOGY.
PA (EHRU-) EHRUCH G.
Query Match 6.2%; Score 74.5; DB 5; Length 3010;
Best Local Similarity 23.8%; Pred. No. 3e+02;
RESULT 857
ID ADF07294 standard; protein; 154 AA.
DE Bacterial polypeptide #3407.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 74; DB 7; Length 154;
Best Local Similarity 26.4%; Pred. No. 5.6;
RESULT 858
ID ABU70365 standard; protein; 231 AA.
DE Human adipocyte bait protein, melatonin receptor_V4.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.2%; Score 74; DB 6; Length 231;
Best Local Similarity 18.5%; Pred. No. 9.9;
RESULT 859
ID ABU70366 standard; protein; 231 AA.
DE Human adipocyte bait protein, melatonin receptor_V5.
PN WO200286122-A2.
PD 31-OCT-2002.
PA (HYBR-) HYBRIGENICS.
Query Match 6.2%; Score 74; DB 6; Length 231;
Best Local Similarity 18.5%; Pred. No. 9.9;
RESULT 860

ID ABB54180 standard; protein; 312 AA.
DE Lactococcus lactis protein y1lg.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.2%; Score 74; DB 5; Length 312;
Best Local Similarity 24.3%; Pred. No. 15;
RESULT 861
ID ADS44483 standard; protein; 312 AA.
DE Bacterial polypeptide #22913.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 74; DB 8; Length 312;
Best Local Similarity 38.3%; Pred. No. 15;
RESULT 862
ID ABO02869 standard; protein; 324 AA.
DE S. pneumoniae type 4 strain protein from coding region #2450.
PN WO200277021-A2.
PD 03-OCT-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.2%; Score 74; DB 6; Length 324;
Best Local Similarity 24.3%; Pred. No. 16;
RESULT 863
ID ABR94027 standard; protein; 332 AA.
DE Novel S. pneumoniae protein sequence, SEQ ID 2662.
PN US6800744-B1.
PD 05-OCT-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 74; DB 8; Length 332;
Best Local Similarity 24.3%; Pred. No. 16;
RESULT 864
ID ABO00448 standard; protein; 342 AA.
DE Novel human polypeptide #35.
PN WO2003032013-A2.
PD 20-MAR-2003.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 74; DB 6; Length 342;
Best Local Similarity 21.2%; Pred. No. 17;
RESULT 865
ID AAR8412 standard; protein; 350 AA.
DE High-affinity melatonin-1a receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 866
ID AAM15786 standard; protein; 350 AA.
DE Melatonin receptor protein.
PN JP09084581-A.
PD 31-MAR-1997.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 867
ID AAM94761 standard; protein; 350 AA.
DE Human melatonin receptor protein mel-1a.
PN EP892046-A2.
PD 20-JUN-1999.
PA (JCRP-) JCR PHARM CO LTD.
Query Match 6.2%; Score 74; DB 2; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 868
ID ABB81840 standard; protein; 350 AA.
DE Human melatonin receptor type 1a protein SEQ ID NO:164.
PN WO200261087-A2.
PD 08-AUG-2002.

PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.2%; Score 74; DB 6; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 869
ID ADO29552 standard; protein; 350 AA.
DE Human GPCR MTNRIA, SEQ ID NO:654.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.2%; Score 74; DB 8; Length 350;
Best Local Similarity 18.5%; Pred. No. 18;
RESULT 870
ID AAM19220 standard; protein; 364 AA.
DE Rat growth hormone secretagogue receptor type Ia.
PN WO9721730-A1.
PD 19-JUN-1997.
PA (MERI) MERCK & CO INC.
Query Match 6.2%; Score 74; DB 2; Length 364;
Best Local Similarity 19.4%; Pred. No. 19;
RESULT 871
ID AAM73179 standard; protein; 366 AA.
DE Staphylococcus aureus protein #2419.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.2%; Score 74; DB 6; Length 366;
Best Local Similarity 21.8%; Pred. No. 19;
RESULT 872
ID ABB55224 standard; protein; 442 AA.
DE Lactococcus lactis protein yred.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.2%; Score 74; DB 5; Length 442;
Best Local Similarity 20.4%; Pred. No. 24;
RESULT 873
ID ADN23927 standard; protein; 485 AA.
DE Bacterial polypeptide #6580.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 74; DB 8; Length 485;
Best Local Similarity 26.2%; Pred. No. 28;
RESULT 874
ID AAY80509 standard; protein; 492 AA.
DE F. lutescens L-lysine:2-oxoglutarate 6-aminotransferase.
PN WO200008170-A1.
PD 17-FEB-2000.
PA (SAOC) MERCIAN CORP.
Query Match 6.2%; Score 74; DB 3; Length 492;
Best Local Similarity 22.5%; Pred. No. 28;
RESULT 875
ID AAG64105 standard; protein; 493 AA.
DE Flavobacterium lutescens L-lysine-6-aminotransferase.
PN WO200148216-A1.
PD 05-JUL-2001.
PA (SAOC) MERCIAN CORP.
Query Match 6.2%; Score 74; DB 4; Length 493;
Best Local Similarity 22.5%; Pred. No. 28;
RESULT 876
ID AAR54067 standard; protein; 1031 AA.
DE Non-A, non-B hepatitis virus gene #6 product.
PN JP06141870-A.
PD 24-MAY-1994.
PA (TOKR-) ZH TOKYO TO KINSHO IGAKU SOGO KENKYUSHO.
PA (SANW) SANWA KAGAKU KENKYUSHO CO.
PA (TOFU) TONEN CORP.
Query Match 6.2%; Score 74; DB 2; Length 1031;
Best Local Similarity 26.2%; Pred. No. 79;

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RESULT 877
ID AAR98362 standard; protein; 1031 AA.
DE 5'UTR/CORE/ENV/NS1/NS2/NS3 from HCV (#6).
PN JF07133291-A.
PD 23-MAY-1995.
PA (TOFU) TONEN CORP.
Query Match 6.2%; Score 74; DB 2; Length 1031;
Best Local Similarity 26.2%; Pred. No. 79;
RESULT 878
ID AAG59839 standard; protein; 120 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 77442.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 120;
Best Local Similarity 20.3%; Pred. No. 4.6;
RESULT 879
ID AAU25578 standard; protein; 192 AA.
DE Human G Protein-Coupled Receptor (GPCR) polypeptide #25.
PN W0200162797-A2.
PD 30-AUG-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.2%; Score 73.5; DB 4; Length 192;
Best Local Similarity 26.3%; Pred. No. 8.8;
RESULT 880
ID ABU44044 standard; protein; 268 AA.
DE Protein encoded by Prokaryotic essential gene #29571.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 73.5; DB 6; Length 268;
Best Local Similarity 19.6%; Pred. No. 14;
RESULT 881
ID AAG32488 standard; protein; 282 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39200.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 282;
Best Local Similarity 28.1%; Pred. No. 15;
RESULT 882
ID ADF05982 standard; protein; 312 AA.
DE Bacterial polypeptide #2095.
PN U86605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.2%; Score 73.5; DB 7; Length 312;
Best Local Similarity 17.4%; Pred. No. 17;
RESULT 883
ID AAG51386 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65212.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 377;
Best Local Similarity 28.1%; Pred. No. 22;
RESULT 884
ID AAG32487 standard; protein; 377 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39199.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 377;
Best Local Similarity 28.1%; Pred. No. 22;
RESULT 885
ID AD075734 standard; protein; 404 AA.
DE Codon optimised hCMV IE1 encoded exons 2 and 4.
PN W02004058166-A2.
PD 15-JUL-2004.
PA (VIC-) VICAL INC.
Query Match 6.2%; Score 73.5; DB 8; Length 404;
Best Local Similarity 19.3%; Pred. No. 25;
RESULT 886
ID AAG51385 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65211.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 442;
Best Local Similarity 28.1%; Pred. No. 28;
RESULT 887
ID AAG32486 standard; protein; 442 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 39198.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 442;
Best Local Similarity 28.1%; Pred. No. 28;
RESULT 888
ID AAG51384 standard; protein; 489 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 65210.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.2%; Score 73.5; DB 3; Length 489;
Best Local Similarity 28.1%; Pred. No. 32;
RESULT 889
ID AAB86544 standard; protein; 491 AA.
DE Human cytomagalovirus strain AD169 IE1 protein.
PN W0200163386-A2.
PD 30-AUG-2001.
PA (KERN/) KERN F.
Query Match 6.2%; Score 73.5; DB 4; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 890
ID ADP12517 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #127.
PN W02004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 891
ID ADP12518 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #128.
PN W02004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 892
ID ADP12513 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #123.
PN W02004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 893
ID ADP12514 standard; protein; 491 AA.
DE Protein encoded by mRNA of the invention #124.
PN W02004042346-A2.
PD 21-MAY-2004.
PA (EXPR-) EXPRESSION DIAGNOSTICS INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 894
ID ADG75725 standard; protein; 491 AA.
DE Wild type hCMV IE1.
PN W02004058166-A2.
PD 15-JUL-2004.
PA (VIC-) VICAL INC.
Query Match 6.2%; Score 73.5; DB 8; Length 491;
Best Local Similarity 19.3%; Pred. No. 32;
RESULT 895
ID ABP73574 standard; protein; 574 AA.
DE Candida albicans essential protein SEQ ID NO 7411.
PN W0200253728-A2.
PD 11-JUL-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.2%; Score 73.5; DB 5; Length 574;
Best Local Similarity 20.8%; Pred. No. 40;
RESULT 896
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ID AD528278 standard; protein; 637 AA.
DE Bacterial polypeptide #17311.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOI/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.2%; Score 73.5; DB 8; Length 637;
Best Local Similarity 28.3%; Pred. No. 46;
RESULT 897
ID ABG29128 standard; protein; 682 AA.
DE Novel human diagnostic protein #29119.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.2%; Score 73.5; DB 4; Length 682;
Best Local Similarity 20.0%; Pred. No. 51;
RESULT 898
ID ABB61737 standard; protein; 1287 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 12003.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (BEKE/) PE CORP NY.
Query Match 6.2%; Score 73.5; DB 4; Length 1287;
Best Local Similarity 18.2%; Pred. No. 1.2e+02;
RESULT 899
ID ADS96670 standard; protein; 1287 AA.
DE Drosophila melanogaster protein, SEQ ID 291.
PN WO200403999-A2.
PD 13-MAY-2004.
PA (SYGN/) SYNGENTA PARTICIPATIONS AG.
Query Match 6.2%; Score 73.5; DB 8; Length 1287;
Best Local Similarity 18.2%; Pred. No. 1.2e+02;
RESULT 900
ID AAR33214 standard; protein; 3033 AA.
DE NANBH virus strain HC-J8 protein.
PN EP532167-A2.
PD 17-MAR-1993.
PA (IMMO) IMMUNO JAPAN INC.
Query Match 6.2%; Score 73.5; DB 2; Length 3033;
Best Local Similarity 27.4%; Pred. No. 4e+02;
RESULT 901
ID AAM20571 standard; protein; 114 AA.
DE H. pylori secreted or periplasmic protein 80257.aa.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.1%; Score 73; DB 2; Length 114;
Best Local Similarity 21.6%; Pred. No. 4.9;
RESULT 902
ID AAU69567 standard; protein; 189 AA.
DE Human G protein-coupled receptor from cDNA Seq.2643.
PN WO200177330-A2.
PD 18-OCT-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.1%; Score 73; DB 5; Length 189;
Best Local Similarity 20.3%; Pred. No. 9.8;
RESULT 903
ID ADC97146 standard; protein; 199 AA.
DE E. faecium protein sequence SEQ ID 6773.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 6.1%; Score 73; DB 7; Length 199;
Best Local Similarity 22.6%; Pred. No. 11;
RESULT 904
ID ABP29367 standard; protein; 249 AA.
DE Streptococcus polypeptide SEQ ID NO 7910.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 6.1%; Score 73; DB 5; Length 249;
Best Local Similarity 24.6%; Pred. No. 14;
RESULT 905
ID AAU87836 standard; protein; 272 AA.
DE T. aureum 7091 elongase TEL01 from plasmid pRAT-4-A1.
PN WO200208401-A2.
PD 31-JAN-2002.
PA (ABBO) ABBOTT LAB.
Query Match 6.1%; Score 73; DB 5; Length 272;
Best Local Similarity 19.9%; Pred. No. 16;
RESULT 906
ID ADH80191 standard; protein; 272 AA.
DE Fungal 7091 elongase protein seq id 75.
PN US2003163845-A1.
PD 28-AUG-2003.
PA (MUKR/) MUKERJI P.
PA (LEON/) EUN-YEONG LEONARD A.
PA (HUAN/) HUANG Y.
PA (PERE/) PEREIRA S L.
Query Match 6.1%; Score 73; DB 8; Length 272;
Best Local Similarity 19.9%; Pred. No. 16;
RESULT 907
ID ABM73154 standard; protein; 290 AA.
DE Staphylococcus aureus protein #2394.
PN WO200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.1%; Score 73; DB 6; Length 290;
Best Local Similarity 23.4%; Pred. No. 18;
RESULT 908
ID ABR47464 standard; protein; 322 AA.
DE Breast cancer associated protein sequence SEQ ID NO.160.
PN WO2003004989-A2.
PD 16-JAN-2003.
PA (MILL-) MILLENIUM PHARM INC.
Query Match 6.1%; Score 73; DB 6; Length 322;
Best Local Similarity 20.6%; Pred. No. 21;
RESULT 909
ID ADN61865 standard; protein; 349 AA.
DE Human novel protein NOV42a.
PN US2004043382-A1.
PD 04-MAR-2004.
PA (PADI/) PADIGARU M.
PA (SPYT/) SPYTEK K A.
PA (SHEN/) SHENOY S G.
PA (TAUP/) TAUPIER R J.
PA (PENR/) PENN C B A.
PA (LILL/) LI L.
PA (ZERR/) ZERRHUSEN B D.
PA (GUSE/) GUSEV V Y.
PA (JIWU/) JI W.
PA (GORM/) GORMAN L.
PA (MILL/) MILLER C E.
PA (KEXU/) KEXUDA R.
PA (PATI/) PATTURAJAN M.
PA (GANG/) GANGOLI E A.
PA (VERN/) VERNET C A M.
PA (GUOX/) GUO X S.
PA (TCHE/) TCHERNEY V T.
PA (FERN/) FERNANDES B R.
PA (CASW/) CASMAN S J.
PA (MALY/) MALYANKAR U M.
PA (GERL/) GERLACH V.
PA (LIUY/) LIU Y.
PA (ANDE/) ANDERSON D W.
PA (SPAD/) SPADERNA S K.
PA (CATI/) CATTERTON E.
PA (LEIT/) LEITE M W.
PA (ZHON/) ZHONG H.
PA (ALSO/) ALSOBROOK J P.
PA (LEPL/) LEPLEY D M.
PA (RIEG/) RIEGER D K.

PA (BURG/) BURGESS C E. 6.1%; Score 73; DB 8; Length 349;
 Query Match
 Best Local Similarity 24.0%; Pred. No. 23;
 RESULT 910
 ID AAM19613 standard; protein; 364 AA.
 DE Rat growth hormone secretagogue receptor type Ia.
 PN W09722004-A1.
 PD 19-JUN-1997.
 PA (MERI) MERCK & CO INC. 6.1%; Score 73; DB 2; Length 364;
 Query Match
 Best Local Similarity 19.4%; Pred. No. 24;
 RESULT 911
 ID AAY54565 standard; protein; 364 AA.
 DE A mouse growth hormone secretagogue receptor.
 PN W0200002918-A1.
 PD 20-JAN-2000.
 PA (MERI) MERCK & CO INC. 6.1%; Score 73; DB 3; Length 364;
 Query Match
 Best Local Similarity 19.4%; Pred. No. 24;
 RESULT 912
 ID AAB97377 standard; protein; 364 AA.
 DE Rat growth hormone secretagogue receptor (GHSR) related protein.
 PN W0200132705-A1.
 PD 10-MAY-2001.
 PA (TAKA) TAKEDA CHEM IND LTD. 6.1%; Score 73; DB 4; Length 364;
 Query Match
 Best Local Similarity 19.4%; Pred. No. 24;
 RESULT 913
 ID ADO29026 standard; protein; 364 AA.
 DE Mouse novel GPCR GHSR, SEQ ID NO:125.
 PN W02004040000-A2.
 PD 13-MAY-2004.
 PA (PRIM-) PRIMAL INC. 6.1%; Score 73; DB 8; Length 364;
 Query Match
 Best Local Similarity 19.4%; Pred. No. 24;
 RESULT 914
 ID AAW77773 standard; protein; 377 AA.
 DE Staphylococcus aureus protein of unknown function.
 PN EF841394-A2.
 PD 13-MAY-1998.
 PA (SMIK) SMITHKLINE BEECHAM CORP. 6.1%; Score 73; DB 2; Length 377;
 Query Match
 Best Local Similarity 23.3%; Pred. No. 26;
 RESULT 915
 ID AAG50065 standard; protein; 415 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63404.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 19.8%; Pred. No. 29;
 RESULT 916
 ID AAG24013 standard; protein; 427 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 27528.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 22.0%; Pred. No. 30;
 RESULT 917
 ID AAG24012 standard; protein; 430 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 27527.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 6.1%; Score 73; DB 3; Length 430;
 RESULT 918
 ID AABU31419 standard; protein; 453 AA.
 DE Protein encoded by Prokaryotic essential gene #16946.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC. 6.1%; Score 73; DB 6; Length 453;
 Query Match
 Best Local Similarity 26.5%; Pred. No. 33;

RESULT 919
 ID AAG50064 standard; protein; 472 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63403.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 19.8%; Pred. No. 35;
 RESULT 920
 ID AAG50063 standard; protein; 474 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 63402.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 19.8%; Pred. No. 35;
 RESULT 921
 ID AAM70313 standard; protein; 490 AA.
 DE Photorhabdus luminescens protein sequence #3410.
 PN W0200294867-A2.
 PD 28-NOV-2002.
 PA (INSP) INST PASTEUR. 6.1%; Score 73; DB 3; Length 474;
 Query Match
 Best Local Similarity 24.6%; Pred. No. 37;
 RESULT 922
 ID AAY33766 standard; protein; 495 AA.
 DE hKv5.1 human brain-specific potassium channel.
 PN W09941372-A1.
 PD 19-AUG-1999.
 PA (ZENE) ZENCA LTD. 6.1%; Score 73; DB 2; Length 495;
 Query Match
 Best Local Similarity 23.2%; Pred. No. 37;
 RESULT 923
 ID ABO63300 standard; protein; 501 AA.
 DE Klebsiella pneumoniae polypeptide seqid 9817.
 PN US6610836-B1.
 PD 26-AUG-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP. 6.1%; Score 73; DB 7; Length 501;
 Query Match
 Best Local Similarity 26.5%; Pred. No. 38;
 RESULT 924
 ID ABB53583 standard; protein; 526 AA.
 DE Human NOV13b protein SEQ ID NO:30.
 PN W0200262999-A2.
 PD 15-AUG-2002.
 PA (CURA-) CURAGEN CORP. 6.1%; Score 73; DB 5; Length 526;
 Query Match
 Best Local Similarity 23.3%; Pred. No. 41;
 RESULT 925
 ID ADH42229 standard; protein; 526 AA.
 DE Novel human protein NOV50d.
 PN W02003102159-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP. 6.1%; Score 73; DB 8; Length 526;
 Query Match
 Best Local Similarity 23.3%; Pred. No. 41;
 RESULT 926
 ID AEU31136 standard; protein; 553 AA.
 DE Protein encoded by Prokaryotic essential gene #16663.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC. 6.1%; Score 73; DB 6; Length 553;
 Query Match
 Best Local Similarity 19.6%; Pred. No. 44;
 RESULT 927
 ID AAG24011 standard; protein; 556 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 27526.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 6.1%; Score 73; DB 3; Length 556;
 RESULT 928
 ID ADO96000 standard; protein; 608 AA.
 DE T cell activation associated protein #89.

PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 19.5%; Score 73; DB 8; Length 608;
RESULT 929
ID ADR99134 standard; protein; 635 AA.
DE Human protein similar to Yeast SSM4, TEB4, SEQ ID 140.
PN W02004078035-A2.
PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match
Best Local Similarity 19.5%; Pred. No. 53; Length 635;
RESULT 930
ID ABB71311 standard; protein; 717 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 40725.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 21.3%; Pred. No. 62; Length 717;
RESULT 931
ID AAM26673 standard; protein; 746 AA.
DE Staphylococcus aureus spoilIR protein.
PN W09726338-A1.
PD 24-JUL-1997.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 23.3%; Score 73; DB 2; Length 746;
RESULT 932
ID AAU37199 standard; protein; 748 AA.
DE Staphylococcus aureus cellular proliferation protein #1369.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELITR-) ELITRA PHARM INC.
Query Match
Best Local Similarity 23.3%; Pred. No. 66; Length 748;
RESULT 933
ID AAM88407 standard; protein; 750 AA.
DE Human adult neural tissue secreted protein s195_10.
PN W09857976-A1.
PD 23-DEC-1998.
PA (GEMY) GENETICS INST INC.
Query Match
Best Local Similarity 19.5%; Pred. No. 66; Length 750;
RESULT 934
ID AAM26672 standard; protein; 788 AA.
DE Staphylococcus aureus spoilIR protein.
PN W09726338-A1.
PD 24-JUL-1997.
PA (SMIK) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 23.3%; Score 73; DB 2; Length 788;
RESULT 935
ID AAU42392 standard; protein; 788 AA.
DE Protein encoded by Prokaryotic essential gene #27919.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELITR-) ELITRA PHARM INC.
Query Match
Best Local Similarity 23.3%; Pred. No. 71; Length 788;
RESULT 936
ID AAU36734 standard; protein; 792 AA.
DE Staphylococcus aureus cellular proliferation protein #904.
PN W0200170955-A2.
PD 27-SEP-2001.
PA (ELITR-) ELITRA PHARM INC.
Query Match
Best Local Similarity 23.3%; Pred. No. 72; Length 792;
RESULT 937
ID ABL19057 standard; protein; 792 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 334.
PN W0200259148-A2.

PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match
Best Local Similarity 23.3%; Score 73; DB 6; Length 792;
RESULT 938
ID AAM73117 standard; protein; 792 AA.
DE Staphylococcus aureus protein #2357.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 23.3%; Score 73; DB 6; Length 792;
RESULT 939
ID AAM68466 standard; protein; 845 AA.
DE Protein encoded by fragment #6 isolated from Hepatitis C virus genome.
PN W09825960-A1.
PD 18-JUN-1998.
PA (INGG-) CENT ING GENETICA & BIOTECNOLOGIA.
Query Match
Best Local Similarity 26.2%; Score 73; DB 2; Length 845;
RESULT 940
ID ADO95946 standard; protein; 910 AA.
DE T cell activation associated protein #62.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 19.5%; Score 73; DB 8; Length 910;
RESULT 941
ID ABG24246 standard; protein; 913 AA.
DE Novel human diagnostic protein #24237.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 19.5%; Score 73; DB 4; Length 913;
RESULT 942
ID AAM51861 standard; protein; 966 AA.
DE Murine polycystic kidney disease protein 2.
PN W0200177331-A1.
PD 18-OCT-2001.
PA (MILL-) MILLENIUM PHARM INC.
Query Match
Best Local Similarity 21.3%; Score 73; DB 5; Length 966;
RESULT 943
ID ABB07819 standard; protein; 966 AA.
DE Mouse polycystic kidney disease protein 2.
PN US2002035056-A1.
PD 21-MAR-2002.
PA (CURT/) CURTIS R A J.
Query Match
Best Local Similarity 21.3%; Score 73; DB 5; Length 966;
RESULT 944
ID ADU76159 standard; protein; 966 AA.
DE Marker gene related amino acid sequence SEQ ID NO:1411.
PN EP1394274-A2.
PD 03-MAR-2004.
PA (GENO-) GENOX RES INC.
Query Match
Best Local Similarity 21.3%; Score 73; DB 8; Length 966;
RESULT 945
ID ABG05866 standard; protein; 971 AA.
DE Novel human diagnostic protein #5857.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 19.5%; Score 73; DB 4; Length 971;
RESULT 946
ID ADR99135 standard; protein; 971 AA.
DE Human protein similar to Yeast SSM4, TEB4, SEQ ID 141.
PN W02004078035-A2.

PD 16-SEP-2004.
PA (FARB) BAYER PHARM CORP.
Query Match 6.1%; Score 73; DB 8; Length 971;
Best Local Similarity 19.5%; Pred. No. 95;
RESULT 947
ID ABG07373. standard; protein; 976 AA.
DE Novel human diagnostic protein #7364.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 73; DB 4; Length 976;
Best Local Similarity 19.5%; Pred. No. 96;
RESULT 948
ID ABU05456 standard; protein; 209 AA.
DE M. tuberculosis and M. leprae marker protein #107.
PN WO200274903-A2.
PD 26-SEP-2002.
PA (INSP) INST PASTEUR.
Query Match 6.1%; Score 72.5; DB 5; Length 209;
Best Local Similarity 22.1%; Pred. No. 13;
RESULT 949
ID ABU15302 standard; protein; 222 AA.
DE Protein encoded by Prokaryotic essential gene #829.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 72.5; DB 6; Length 222;
Best Local Similarity 20.5%; Pred. No. 14;
RESULT 950
ID ABB53879 standard; protein; 307 AA.
DE Lactococcus lactis protein yf5g.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 72.5; DB 5; Length 307;
Best Local Similarity 22.9%; Pred. No. 22;
RESULT 951
ID ABB53675 standard; protein; 325 AA.
DE Lactococcus lactis protein ydhb.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.1%; Score 72.5; DB 5; Length 325;
Best Local Similarity 25.9%; Pred. No. 24;
RESULT 952
ID ADH81677 standard; protein; 353 AA.
DE Enterococcus faecalis polypeptide #2157.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 72.5; DB 7; Length 353;
Best Local Similarity 21.5%; Pred. No. 27;
RESULT 953
ID ADH87557 standard; protein; 359 AA.
DE Enterococcus faecalis polypeptide #2037.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 6.1%; Score 72.5; DB 7; Length 359;
Best Local Similarity 25.0%; Pred. No. 27;
RESULT 954
ID AAR37264 standard; protein; 389 AA.
DE Oxytocin receptor.
PN EP542424-A1.
PD 19-MAY-1993.
PA (ROHT) ROHTO PHARM CO LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 955
ID AAW23832 standard; protein; 389 AA.
DE Human oxytocin receptor.

PN EP811684-A2.
PD 10-DEC-1997.
PA (ROHT) ROHTO PHARM CO LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 956
ID AAM40217 standard; protein; 389 AA.
DE Human polypeptide SEQ ID NO 3362.
PN WO200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 6.1%; Score 72.5; DB 4; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 957
ID ABR81865 standard; protein; 389 AA.
DE Human oxytocin receptor protein SEQ ID NO:215.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 6.1%; Score 72.5; DB 6; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 958
ID AAR38317 standard; protein; 389 AA.
DE Human oxytocin receptor protein.
PN WO2003064402-A1.
PD 07-AUG-2003.
PA (PFIZ) PFIZER LTD.
PA (PFIZ) PFIZER INC.
Query Match 6.1%; Score 72.5; DB 6; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 959
ID ADP12125 standard; protein; 389 AA.
DE Human oxytocin receptor (OXTR) protein SEQ ID NO:2.
PN WO2003093816-A2.
PD 13-NOV-2003.
PA (FARB) BAYER AG.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 960
ID ADI03915 standard; protein; 389 AA.
DE Human oxytocin receptor polypeptide.
PN WO2004000993-A2.
PD 31-DEC-2003.
PA (UYOU-) UNIV QUEBEC A MONTREAL.
PA (UYMO-) UNIV MONTREAL CENT HOSPITALIER.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 961
ID ADO29590 standard; protein; 389 AA.
DE Human GPCR OXTR, SEQ ID NO:692.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 6.1%; Score 72.5; DB 8; Length 389;
Best Local Similarity 24.5%; Pred. No. 31;
RESULT 962
ID AAR58665 standard; protein; 448 AA.
DE Bovine PACAP receptor type IB mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 448;
Best Local Similarity 29.6%; Pred. No. 37;
RESULT 963
ID AAR58663 standard; protein; 476 AA.
DE Bovine PACAP receptor type 1A mature protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 476;
Best Local Similarity 29.6%; Pred. No. 40;
RESULT 964
ID AAR58657 standard; protein; 485 AA.

DE Bovine PACAP receptor type 1B protein.
PD EP618291-A2.
PN 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 485;
Best Local Similarity 29.6%; Pred. No. 42;
RESULT 965
ID AARS865 standard; protein; 513 AA.
DE Bovine PACAP receptor type 1A protein.
PD EP618291-A2.
PN 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 6.1%; Score 72.5; DB 2; Length 513;
Best Local Similarity 29.6%; Pred. No. 45;
RESULT 966
ID ADN19765 standard; protein; 522 AA.
DE Bacterial polypeptide #2418.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAR/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 6.1%; Score 72.5; DB 8; Length 522;
Best Local Similarity 22.5%; Pred. No. 46;
RESULT 967
ID AD181620 standard; protein; 769 AA.
DE C. elegans protein similar to Pfam PF00023.
PN US2004009537-A1.
PD 15-JAN-2004.
PA (ROOS/) ROOS J.
PA (STAU/) STAUDERMAN K.
PA (VELI/) VELICELEBI G.
Query Match 6.1%; Score 72.5; DB 8; Length 769;
Best Local Similarity 20.2%; Pred. No. 79;
RESULT 968
ID ABB05429 standard; protein; 848 AA.
DE Arabidopsis thaliana ABH1 protein SEQ ID NO:2.
PN WO200196585-A2.
PD 20-DEC-2001.
PA (REGC) UNIV CALIFORNIA.
Query Match 6.1%; Score 72.5; DB 5; Length 848;
Best Local Similarity 22.3%; Pred. No. 90;
RESULT 969
ID AAE31528 standard; protein; 848 AA.
DE Arabidopsis thaliana protein used to isolate rice CBP80 orthologues.
PN WO200281696-A2.
PD 17-OCT-2002.
PA (SYGN) SYNGENTA PARTICIPATIONS AG.
Query Match 6.1%; Score 72.5; DB 6; Length 848;
Best Local Similarity 22.3%; Pred. No. 90;
RESULT 970
ID ABU25159 standard; protein; 851 AA.
DE Protein encoded by Prokaryotic essential gene #10686.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.1%; Score 72.5; DB 6; Length 851;
Best Local Similarity 20.5%; Pred. No. 91;
RESULT 971
ID AAR34580 standard; protein; 3010 AA.
DE Human hepatitis C virus gene encoded polypeptide.
PN EP541089-A2.
PD 12-MAY-1993.
PA (SANM) SANMA KAGAKU KENKYUSHO CO.
Query Match 6.1%; Score 72.5; DB 2; Length 3010;
Best Local Similarity 23.7%; Pred. No. 5.2e+02;
RESULT 972
ID ADO96378 standard; protein; 208 AA.
DE T cell activation associated protein #278.
PN WO2004058805-A2.
PD 15-JUL-2004.

PA (ASAH-) ASAHI KASEI PHARMA CORP.
Query Match 6.0%; Score 72; DB 8; Length 208;
Best Local Similarity 20.8%; Pred. No. 15;
RESULT 973
ID ABB48543 standard; protein; 306 AA.
DE Listeria monocytogenes protein #1247.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match 6.0%; Score 72; DB 5; Length 306;
Best Local Similarity 21.0%; Pred. No. 25;
RESULT 974
ID ABU3432 standard; protein; 317 AA.
DE Protein encoded by Prokaryotic essential gene #24959.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 317;
Best Local Similarity 23.5%; Pred. No. 26;
RESULT 975
ID AAB53392 standard; protein; 334 AA.
DE Human colon cancer antigen protein sequence SEQ ID NO:932.
PN WO200055351-A1.
PD 21-SEP-2000.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 72; DB 3; Length 334;
Best Local Similarity 28.8%; Pred. No. 28;
RESULT 976
ID AAY87505 standard; protein; 370 AA.
DE Human G coupled-protein receptor, hGR3.
PN WO200017641-A1.
PD 30-MAR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 370;
Best Local Similarity 21.8%; Pred. No. 33;
RESULT 977
ID AAW20731 standard; protein; 375 AA.
DE H. pylori inner membrane protein, 06cp1118orf6.
PN WO9640893-A1.
PD 19-DEC-1996.
PA (ASTR) ASTRA AB.
Query Match 6.0%; Score 72; DB 2; Length 375;
Best Local Similarity 20.9%; Pred. No. 33;
RESULT 978
ID ABU19932 standard; protein; 396 AA.
DE Protein encoded by Prokaryotic essential gene #5459.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 72; DB 6; Length 396;
Best Local Similarity 21.6%; Pred. No. 36;
RESULT 979
ID ABG25051 standard; protein; 414 AA.
DE Novel human diagnostic protein #25042.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSR-) HYSRQ INC.
Query Match 6.0%; Score 72; DB 4; Length 414;
Best Local Similarity 22.6%; Pred. No. 38;
RESULT 980
ID AAG50203 standard; protein; 427 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63592.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 427;
Best Local Similarity 22.0%; Pred. No. 40;
RESULT 981
ID AAG50202 standard; protein; 430 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63591.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 72; DB 3; Length 430;
Best Local Similarity 22.0%; Pred. No. 40;

RESULT 982
ID ABM72825 standard; protein: 447 AA.
DE Staphylococcus aureus protein #2065.
PN W020029486-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match
Best Local Similarity 23.9%; Pred. No. 42; Length 447;
RESULT 983
ID ABB62902 standard; protein: 448 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 15498.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEXE) PE CORP NV.
Query Match
Best Local Similarity 25.1%; Pred. No. 43; Length 448;
RESULT 984
ID ABU16913 standard; protein: 453 AA.
DE Pathogen specific antigen related staphylococcal protein SEQ ID NO 59.
PN W0200259148-A2.
PD 01-AUG-2002.
PA (CIST-) CISTEM BIOTECHNOLOGIES GMBH.
Query Match
Best Local Similarity 23.9%; Pred. No. 43; Length 453;
RESULT 985
ID ABU16441 standard; protein: 453 AA.
DE Protein encoded by prokaryotic essential gene #1968.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 23.9%; Pred. No. 43; Length 453;
RESULT 986
ID AON73057 standard; protein: 468 AA.
DE Thale cress protein upregulated in E2Fa/Dpa expressing plants SeqID 952.
PN W02004035798-A2.
PD 29-APR-2004.
PA (CROP-) CROPDDESIGN NV.
Query Match
Best Local Similarity 21.8%; Pred. No. 45; Length 468;
RESULT 987
ID AAG16338 standard; protein: 495 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16945.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 21.3%; Pred. No. 49; Length 495;
RESULT 988
ID AAG16337 standard; protein: 497 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16944.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 21.3%; Pred. No. 49; Length 497;
RESULT 989
ID AAG16336 standard; protein: 507 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 16943.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 21.3%; Pred. No. 51; Length 507;
RESULT 990
ID ADB23568 standard; protein: 543 AA.
DE Bacterial polypeptide #12601.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 18.6%; Pred. No. 56; Length 543;

RESULT 991
ID ABU25738 standard; protein: 552 AA.
DE Protein encoded by prokaryotic essential gene #11265.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 19.5%; Pred. No. 57; Length 552;
RESULT 992
ID AAG50201 standard; protein: 556 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 63590.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match
Best Local Similarity 22.0%; Pred. No. 58; Length 556;
RESULT 993
ID ADB69383 standard; protein: 594 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID1189.
PN W02003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match
Best Local Similarity 20.8%; Pred. No. 63; Length 594;
RESULT 994
ID ABB97202 standard; protein: 696 AA.
DE Tumour-associated antigenic target protein TAR247 SEQ ID NO:84.
PN W02003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.8%; Pred. No. 79; Length 696;
RESULT 995
ID ABB97201 standard; protein: 696 AA.
DE Tumour-associated antigenic target protein TAR225 SEQ ID NO:83.
PN W02003024392-A2.
PD 27-MAR-2003.
PA (GETH) GENENTECH INC.
Query Match
Best Local Similarity 20.8%; Pred. No. 79; Length 696;
RESULT 996
ID ABB81969 standard; protein: 696 AA.
DE Human GPCR XPR1 protein SEQ ID NO:424.
PN W0200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 20.8%; Pred. No. 79; Length 696;
RESULT 997
ID ADB67652 standard; protein: 696 AA.
DE Human xenotropic polytropic retrovirus receptor, SEQ ID 21.
PN W02003072824-A1.
PD 04-SEP-2003.
PA (SANY) SANKYO CO LTD.
Query Match
Best Local Similarity 20.8%; Pred. No. 79; Length 696;
RESULT 998
ID ADB67652 standard; protein: 696 AA.
DE T cell activation associated protein #279.
PN W02004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match
Best Local Similarity 20.8%; Pred. No. 79; Length 696;
RESULT 999
ID ABM69179 standard; protein: 724 AA.
DE Photobacterium luminescens protein sequence #2276.
PN W0200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match
Best Local Similarity 21.3%; Pred. No. 83; Length 724;

RESULT 1000
ID AAB46702 standard; protein: 741 AA.
DE P. falciparum DNA polymerase protein fragment SEQ ID NO 11.
PN W020007535-A2.
PD 14-DEC-2000.
PA (DECO-) DECODE GENETICS BHF.
Query Match 6.0%; Score 72; DB 4; Length 741;
Best Local Similarity 30.4%; Pred. No. 86;
RESULT 1001
ID AAM47977 standard; protein: 788 AA.
DE Human HARG.
PN CN1315342-A.
PD 03-OCT-2001.
PA (BODA-) BODAO GENE TECHNOLOGY CO LTD SHANGHAI.
Query Match 6.0%; Score 72; DB 5; Length 788;
Best Local Similarity 26.3%; Pred. No. 93;
RESULT 1002
ID ABB58917 standard; protein: 1275 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 3543.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE-) PE CORP NY.
Query Match 6.0%; Score 72; DB 4; Length 1275;
Best Local Similarity 19.0%; Pred. No. 1.8e+02;
RESULT 1003
ID AAY70064 standard; protein: 2307 AA.
DE Recombinant fusion pHCAP-1 polypeptide.
PN W0200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.6%; Pred. No. 4.1e+02;
RESULT 1004
ID AAY70065 standard; protein: 2307 AA.
DE Recombinant fusion pHCAP-3 polypeptide.
PN W0200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.6%; Pred. No. 4.1e+02;
RESULT 1005
ID AAY70066 standard; protein: 2307 AA.
DE Recombinant fusion pHCAP-4 polypeptide.
PN W0200008469-A1.
PD 17-FEB-2000.
PA (AGOU-) AGOURON PHARM INC.
Query Match 6.0%; Score 72; DB 3; Length 2307;
Best Local Similarity 23.6%; Pred. No. 4.1e+02;
RESULT 1006
ID AAM93791 standard; protein: 208 AA.
DE Human polypeptide, SEQ ID NO: 3817.
PN EP1130094-A2.
PD 05-SEP-2001.
PA (HELI-) HELIX RES INST.
Query Match 6.0%; Score 71.5; DB 4; Length 208;
Best Local Similarity 25.2%; Pred. No. 17;
RESULT 1007
ID ADL31784 standard; protein: 208 AA.
DE Human protein encoded by a full length cDNA clone SeqID 3817.
PN EP136543-A2.
PD 10-MAR-2004.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 6.0%; Score 71.5; DB 8; Length 208;
Best Local Similarity 25.2%; Pred. No. 17;
RESULT 1008
ID AAG56417 standard; protein: 209 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 72517.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 209;
Best Local Similarity 25.6%; Pred. No. 17;
RESULT 1009
ID AAG56416 standard; protein: 216 AA.

DE Arabidopsis thaliana protein fragment SEQ ID NO: 72516.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 216;
Best Local Similarity 25.6%; Pred. No. 18;
RESULT 1010
ID AAG16922 standard; protein: 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 17750.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 6.0%; Score 71.5; DB 3; Length 218;
Best Local Similarity 42.4%; Pred. No. 18;
RESULT 1011
ID ABB53486 standard; protein: 301 AA.
DE Lactococcus lactis protein yb1G.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match 6.0%; Score 71.5; DB 5; Length 301;
Best Local Similarity 26.5%; Pred. No. 28;
RESULT 1012
ID AAM37976 standard; protein: 342 AA.
DE Kaposi's sarcoma associated herpesvirus G protein-coupled receptor.
PN W03815288-A1.
PD 16-APR-1998.
PA (CORR-) CORNELL RES FOUND INC.
Query Match 6.0%; Score 71.5; DB 2; Length 342;
Best Local Similarity 22.2%; Pred. No. 34;
RESULT 1013
ID ADG87423 standard; protein: 348 AA.
DE Meloidogyne incognita PLK1 protein.
PN US2003150017-A1.
PD 07-AUG-2003.
PA (MESA/) MESA J R B.
PA (GRAH/) GRAHAM M W.
PA (PAIR/) FAIRBAIN D J.
Query Match 6.0%; Score 71.5; DB 7; Length 348;
Best Local Similarity 21.0%; Pred. No. 34;
RESULT 1014
ID ADR40542 standard; protein: 363 AA.
DE Ovine MLK protein.
PN US2004161823-A1.
PD 19-AUG-2004.
PA (PEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANTHAN C S.
PA (HAWK/) HAWKEN D R.
Query Match 6.0%; Score 71.5; DB 8; Length 363;
Best Local Similarity 23.1%; Pred. No. 36;
RESULT 1015
ID AAR88410 standard; protein: 366 AA.
DE High-affinity melatonin-1a receptor.
PN W0535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match 6.0%; Score 71.5; DB 2; Length 366;
Best Local Similarity 23.1%; Pred. No. 37;
RESULT 1016
ID ABR03456 standard; protein: 382 AA.
DE Angiogenesis-associated human protein sequence #1.
PN W0200279492-A2.
PD 10-OCT-2002.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 39;
RESULT 1017
ID ABB58069 standard; protein: 382 AA.
DE Human G-protein coupled receptor GAVEL.
PN W0200295056-A2.
PD 28-NOV-2002.
PA (AVET-) AVENTIS PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 382;
Best Local Similarity 22.3%; Pred. No. 39;

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RESULT 1018
ID ABR59277 standard; protein; 382 AA.
DE Human Edg1 receptor.
PN WO2003006503-A1.
PD 23-JAN-2003.
PA (CERE-) CERETEK.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 6; Length 382;
RESULT 1019
ID ABU08809 standard; protein; 382 AA.
DE Human EDG-1 protein.
PN US2002155512-A1.
PD 24-OCT-2002.
PA (RIGR-) RIGEL PHARM INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 6; Length 382;
RESULT 1020
ID ABR59701 standard; protein; 382 AA.
DE Human endothelial differentiation sphingolipid GPCR 1.
PN WO2003029277-A2.
PD 10-APR-2003.
PA (RIGR-) RIGEL PHARM INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 6; Length 382;
RESULT 1021
ID ABR81876 standard; protein; 382 AA.
DE Human sphingolipid receptor Edg1 protein SEQ ID NO:237.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 6; Length 382;
RESULT 1022
ID ADB6762 standard; protein; 382 AA.
DE Human EDG1, SEQ ID 31.
PN WO2003072824-A1.
PD 04-SEP-2003.
PA (SANY) SANKYO CO LTD.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 7; Length 382;
RESULT 1023
ID ADC40477 standard; protein; 382 AA.
DE Protein of human EDG-1.
PN WO2003052096-A1.
PD 26-JUN-2003.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 7; Length 382;
RESULT 1024
ID ADN36884 standard; protein; 382 AA.
DE Cancer/angiogenesis/fibroblast-related polypeptide, SEQ ID NO:2.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 7; Length 382;
RESULT 1025
ID ABM85457 standard; protein; 382 AA.
DE Human protein sequence hCP1650135.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGES DISCOVERY.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 7; Length 382;
RESULT 1026
ID ADJ45541 standard; protein; 382 AA.
DE LXR-1 ligand induced transcript seq id 72.
PN US2004023276-A1.
PD 05-FEB-2004.
PA (WARD/) WARD T R.
PA (MAOM/) MAO M.
PA (LINS/) LINSLEY P S.
PA (LUND/) LUND E.

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Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 8; Length 382;
RESULT 1027
ID ADR67022 standard; protein; 382 AA.
DE Human cancer associated protein sequence SEQ ID NO:68.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGES DISCOVERY INC.
Query Match
Best Local Similarity 22.3%; Pred. No. 39; Length 382;
Score 71.5; DB 8; Length 382;
RESULT 1028
ID ADN19614 standard; protein; 383 AA.
DE Bacterial polypeptide #2267.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOT/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
Best Local Similarity 22.0%; Pred. No. 39; Length 383;
Score 71.5; DB 8; Length 383;
RESULT 1029
ID ABB05226 standard; protein; 390 AA.
DE Catostomus commersoni isotocin receptor protein SEQ ID NO:3.
PN WO200192296-A2.
PD 06-DEC-2001.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 22.2%; Pred. No. 40; Length 390;
Score 71.5; DB 5; Length 390;
RESULT 1030
ID ADM83141 standard; protein; 394 AA.
DE Rat vesicle membrane protein (VMP)2.
PN US2003175787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match
Best Local Similarity 22.7%; Pred. No. 41; Length 394;
Score 71.5; DB 7; Length 394;
RESULT 1031
ID ABB48023 standard; protein; 435 AA.
DE Listeria monocytogenes protein #727.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP) INSR PASTEUR.
Query Match
Best Local Similarity 21.4%; Pred. No. 47; Length 435;
Score 71.5; DB 5; Length 435;
RESULT 1032
ID AAR22000 standard; protein; 441 AA.
DE Partial M17 antigen from Region II, encoded by PCR prod.
PN WO9203457-A.
PD 05-MAR-1992.
PA (REGC) UNIV CALIFORNIA.
Query Match
Best Local Similarity 22.6%; Pred. No. 48; Length 441;
Score 71.5; DB 2; Length 441;
RESULT 1033
ID ABR75877 standard; protein; 470 AA.
DE Human secretory polypeptide SPTM SEQ ID NO 1061.
PN WO200283876-A2.
PD 24-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 22.4%; Pred. No. 52; Length 470;
Score 71.5; DB 6; Length 470;
RESULT 1034
ID ABU26033 standard; protein; 524 AA.
DE Protein encoded by Prokaryotic essential gene #11560.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 26.6%; Pred. No. 61; Length 524;
Score 71.5; DB 6; Length 524;
RESULT 1035
ID ABJ37074 standard; protein; 565 AA.
DE Human breast cancer / ovarian cancer related protein #50.

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PN W02003000012-A2.
PD 03-JAN-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 565;
Best Local Similarity 22.4%; Pred. No. 67;
RESULT 1036
ID AAW51244 standard; protein; 568 AA.
DE Human calcitonin receptor.
PN W09821242-A1.
PD 23-MAY-1998.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 6.0%; Score 71.5; DB 2; Length 568;
Best Local Similarity 22.4%; Pred. No. 68;
RESULT 1037
ID ABU16392 standard; protein; 603 AA.
DE Protein encoded by Prokaryotic essential gene #1919.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (BLIT-) ELITRA PHARM INC.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 74;
RESULT 1038
ID ABM72619 standard; protein; 603 AA.
DE Staphylococcus aureus protein #1859.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 6.0%; Score 71.5; DB 6; Length 603;
Best Local Similarity 21.3%; Pred. No. 74;
RESULT 1039
ID ADM43215 standard; protein; 697 AA.
DE Human methionine synthase reductase del Arg 559 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1040
ID ADM4317 standard; protein; 697 AA.
DE Human methionine synthase reductase del Leu 576 variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 697;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1041
ID AAB07591 standard; protein; 698 AA.
DE A human methionine synthase reductase polypeptide.
PN W0200042196-A2.
PD 20-JUL-2000.
PA (UYMC-) UNIV MCGILL.
Query Match 6.0%; Score 71.5; DB 3; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1042
ID ABG00883 standard; protein; 698 AA.
DE Novel human diagnostic protein #874.
PN W0200175067-A2.
PD 11-OCT-2001.
PA (HYSR-) HYSEQ INC.
Query Match 6.0%; Score 71.5; DB 4; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1043
ID ADM43211 standard; protein; 698 AA.
DE Human methionine synthase reductase Met2211e variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1044
ID ADM43213 standard; protein; 698 AA.
DE Human methionine synthase reductase Cys377Yr variant.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1045
ID ADM43207 standard; protein; 698 AA.
DE Human wild-type methionine synthase reductase.
PN US2003082676-A1.
PD 01-MAY-2003.
PA (GRAV/) GRAVEL R A.
PA (ROZE/) ROZEN R.
PA (LECL/) LECLERC D.
PA (WILS/) WILSON A.
PA (ROSE/) ROSENBLATT D.
Query Match 6.0%; Score 71.5; DB 7; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1046
ID ADO39857 standard; protein; 698 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1520.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 698;
Best Local Similarity 22.8%; Pred. No. 90;
RESULT 1047
ID ADO39858 standard; protein; 725 AA.
DE Human myocardial infarction-associated gene derived protein, SEQ ID 1521.
PN W02004058052-A2.
PD 15-JUL-2004.
PA (APPL-) APPLERA CORP.
Query Match 6.0%; Score 71.5; DB 8; Length 725;
Best Local Similarity 22.8%; Pred. No. 95;
RESULT 1048
ID AAY51606 standard; protein; 890 AA.
DE Human wml protein.
PN DE19845277-Cl.
PD 09-MAR-2000.
PA (UYMC-) UNIV MÜNCHEN MAXIMILIANS LUDWIG.
Query Match 6.0%; Score 71.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.3e+02;
RESULT 1049
ID ABB78282 standard; protein; 890 AA.
DE Amino acid sequence of human wolframin polypeptide.
PN W0200263307-A2.
PD 15-AUG-2002.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 6.0%; Score 71.5; DB 5; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.3e+02;
RESULT 1050
ID ADD46013 standard; protein; 890 AA.
DE Human Protein O76024, SEQ ID NO 11685.
PN W02003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 6.0%; Score 71.5; DB 7; Length 890;
Best Local Similarity 23.8%; Pred. No. 1.3e+02;

RESULT 1051
ID ADF63127 standard; protein; 890 AA.
DE Human M953 protein sequence SEQ ID NO:97.
PN WO2003083047-A2.
PD 09-OCT-2003.
PA (EXEL-) EXELIXIS INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 890;
Pred. No. 1.3e+02;
RESULT 1052
ID ADL2689 standard; protein; 2245 AA.
DE Human disease detection and treatment (MDDT) protein - SEQ ID 138.
PN WO2003062379-A2.
PD 31-JUL-2003.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2245;
Pred. No. 4.6e+02;
RESULT 1053
ID AAB42192 standard; protein; 2405 AA.
DE Human ORFX ORF1956 polypeptide sequence SEQ ID NO:3912.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 3; Length 2405;
Pred. No. 5e+02;
RESULT 1054
ID ABB11404 standard; peptide; 2560 AA.
DE Human FLAMINGO 1 homologue, SEQ ID NO:1774.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 4; Length 2560;
Pred. No. 5.5e+02;
RESULT 1055
ID ABU11556 standard; protein; 2894 AA.
DE Human MDDT polypeptide SEQ ID 503.
PN WO200279449-A2.
PD 10-OCT-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 2894;
Pred. No. 6.5e+02;
RESULT 1056
ID AAU07054 standard; protein; 2923 AA.
DE Human Flamingo protein encoded by cDNA splice variant.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIX) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 4; Length 2923;
Pred. No. 6.6e+02;
RESULT 1057
ID AAM50866 standard; protein; 2923 AA.
DE Cadherin EGF LAG seven-pass G-type receptor 2, basal cell marker.
PN WO200208765-A2.
PD 31-JAN-2002.
PA (STRD) UNIV STANFORD.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 5; Length 2923;
Pred. No. 6.6e+02;
RESULT 1058
ID ABP82018 standard; protein; 2923 AA.
DE Human GPCR CELSR2 protein SEQ ID NO:524.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 6; Length 2923;
Pred. No. 6.6e+02;
RESULT 1059
ID AOC15499 standard; protein; 2923 AA.
DE Human cadherin EGF LAG seven-pass G-type receptor 2.
PN US2003086934-A1.
PD 08-MAY-2003.
PA (BOTS/) BOTSTEIN D.
PA (BROW/) BROWN P O.
PA (PERO/) PEROU C M.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 3011;
Pred. No. 6.9e+02;
RESULT 1060
ID ADE54411 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 214.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2923;
Pred. No. 6.6e+02;
RESULT 1061
ID ADE54407 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 210.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2923;
Pred. No. 6.6e+02;
RESULT 1062
ID ADE54411 standard; protein; 2923 AA.
DE Human Protein XP_042739, SEQ ID NO 214.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GENO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 7; Length 2923;
Pred. No. 6.6e+02;
RESULT 1063
ID ADO29245 standard; protein; 2923 AA.
DE Human GPCR CELSR2, SEQ ID NO:346.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 8; Length 2923;
Pred. No. 6.6e+02;
RESULT 1064
ID AAU74826 standard; protein; 2936 AA.
DE Human REPTR 9 protein.
PN WO200198354-A2.
PD 27-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 5; Length 2936;
Pred. No. 6.6e+02;
RESULT 1065
ID AAU07053 standard; protein; 2956 AA.
DE Human Flamingo polypeptide.
PN WO200161003-A1.
PD 23-AUG-2001.
PA (SMIX) SMITHKLINE BEECHAM PLC.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 4; Length 2956;
Pred. No. 6.7e+02;
RESULT 1066
ID AAR34468 standard; protein; 3011 AA.
DE Encoded by full-length Hepatitis C virus clone JKI-B.
PN JP05068562-A.
PD 23-MAR-1993.
PA (SANW) SANWA KAGAKU KENKUSHO CO.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 3011;
Pred. No. 6.9e+02;
RESULT 1067
ID AAR31621 standard; protein; 3011 AA.
DE Hepatitis C virus (HCV) polypeptide.
PN WO9300365-A2.
PD 07-JAN-1993.
PA (CHIR) CHIRON CORP.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 2; Length 3011;
Pred. No. 6.9e+02;

RESULT 1068
ID ABB67866 standard; protein; 5303 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 30390.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match
Best Local Similarity 6.0%; Score 71.5; DB 4; Length 5303;
RESULT 1069
ID ABB06793 standard; protein; 198 AA.
DE Human transmembrane 4 protein 22 SEQ ID NO:2.
PN CN1327990-A.
PD 26-DEC-2001.
PA (BODE-) BODE GENE DEV CO LTD SHANGHAI.
Query Match
Best Local Similarity 5.9%; Score 71; DB 5; Length 198;
RESULT 1070
ID ABR58398 standard; protein; 240 AA.
DE Human NOV17a.
PN W02003029423-A2.
PD 10-APR-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 6; Length 240;
RESULT 1071
ID ABB26255 standard; protein; 295 AA.
DE Streptococcus polypeptide SEQ ID NO 1686.
PN W0200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match
Best Local Similarity 5.9%; Score 71; DB 5; Length 295;
RESULT 1072
ID AAG72952 standard; protein; 310 AA.
DE Human olfactory receptor data exploratorium sequence, SEQ ID NO: 2634.
PN W0200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match
Best Local Similarity 5.9%; Score 71; DB 4; Length 310;
RESULT 1073
ID AAR48717 standard; protein; 312 AA.
DE G-protein coupled human interleukin-8 receptor protein.
PN W03405695-A1.
PD 17-MAR-1994.
PA (UYNY) UNIV NEW YORK STATE.
Query Match
Best Local Similarity 5.9%; Score 71; DB 2; Length 312;
RESULT 1074
ID AAM02689 standard; peptide; 312 AA.
DE G-protein coupled human interleukin-8 receptor.
PN US5508384-A.
PD 16-APR-1996.
PA (UYNY) UNIV NEW YORK STATE.
Query Match
Best Local Similarity 5.9%; Score 71; DB 2; Length 312;
RESULT 1075
ID AAG72169 standard; protein; 312 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1850.
PN W0200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
PA (YEDA) YEDA RES & DEV CO LTD.
Query Match
Best Local Similarity 5.9%; Score 71; DB 4; Length 312;
RESULT 1076
ID AAG72377 standard; protein; 312 AA.
DE Human OR-like polypeptide query sequence, SEQ ID NO: 2058.
PN W0200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.

PA (YEDA) YEDA RES & DEV CO LTD.
Query Match
Best Local Similarity 5.9%; Score 71; DB 4; Length 312;
RESULT 1077
ID ABB54394 standard; protein; 391 AA.
DE Lactococcus lactis protein Yk11.
PN FR2807446-A1.
PD 12-OCT-2001.
PA (INRG) INRA INST NAT RECH AGRONOMIQUE.
Query Match
Best Local Similarity 5.9%; Score 71; DB 5; Length 391;
RESULT 1078
ID ABB48413 standard; protein; 423 AA.
DE Listeria monocytogenes protein #1117.
PN W0200177335-A2.
PD 18-OCT-2001.
PA (INSP) INST PASTEUR.
Query Match
Best Local Similarity 5.9%; Score 71; DB 5; Length 423;
RESULT 1079
ID ADL05302 standard; protein; 423 AA.
DE M. catarrhalis protein #1068.
PN US6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 423;
RESULT 1080
ID AD095142 standard; protein; 444 AA.
DE Novel NOVX protein sequence #185.
PN W02003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 7; Length 444;
RESULT 1081
ID AD095144 standard; protein; 444 AA.
DE Novel NOVX protein sequence #186.
PN W02003040325-A2.
PD 15-MAY-2003.
PA (CURA-) CURAGEN CORP.
Query Match
Best Local Similarity 5.9%; Score 71; DB 7; Length 444;
RESULT 1082
ID ADP29417 standard; protein; 455 AA.
DE Human secreted protein SEQ ID #184.
PN W02004035732-A2.
PD 29-APR-2004.
PA (FIVE-) FIVE PRIME THERAPEUTICS INC.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 455;
RESULT 1083
ID ABU19912 standard; protein; 457 AA.
DE Protein encoded by Prokaryotic essential gene #5439.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match
Best Local Similarity 5.9%; Score 71; DB 6; Length 457;
RESULT 1084
ID AD124575 standard; protein; 470 AA.
DE Human endogenous 5HT2A serotonin receptor.
PN US2003224442-A1.
PD 04-DEC-2003.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
PA (LIAM/) LIAM C W.
PA (RUSS/) RUSSO J F.
PA (THOM/) THOMSEN W J.
Query Match
Best Local Similarity 5.9%; Score 71; DB 8; Length 470;
RESULT 1085
ID AAR37659 standard; protein; 471 AA.

DE Sequence encoded by cDNA.
 PN WO9311257-A2.
 PD 10-JUN-1993.
 PA (BOEH) BOEHRINGER INGELHEIM INT GMBH.
 DE Human serotonin 2A receptor.
 Query Match 5.9%; Score 71; DB 2; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1086
 ID AAM23781 standard; protein; 471 AA.
 DE Human serotonin 5-HT2 receptor protein.
 PN US5661024-A.
 PD 26-AUG-1997.
 PA (SYNA-) SYNAPTIC PHARM CORP.
 DE Human serotonin 5-HT2 receptor protein.
 Query Match 5.9%; Score 71; DB 2; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1087
 ID AAM77107 standard; protein; 471 AA.
 DE Human 5-HT2A serotonin receptor.
 PN WO9838217-A1.
 PD 03-SEP-1998.
 PA (TEIT/) TEITLER M.
 PA (HERR/) HERRICK-DAVIS K.
 PA (EGAN/) EGAN C C.
 DE Human 5-HT2A serotonin receptor.
 Query Match 5.9%; Score 71; DB 2; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1088
 ID AAY90640 standard; protein; 471 AA.
 DE Human G protein-coupled receptor 5HT-2A (serotonin receptor).
 PN WO200022129-A1.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 DE Human G protein-coupled receptor 5HT-2A.
 Query Match 5.9%; Score 71; DB 3; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1089
 ID AAY90675 standard; protein; 471 AA.
 DE Human mutant G protein-coupled receptor 5HT-2A.
 PN WO200022129-A1.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 DE Human mutant G protein-coupled receptor 5HT-2A.
 Query Match 5.9%; Score 71; DB 3; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1090
 ID ABB07978 standard; protein; 471 AA.
 DE Human 5-HT2 receptor sequence.
 PN US6383762-B1.
 PD 07-MAY-2002.
 PA (SYNA-) SYNAPTIC PHARM CORP.
 DE Human 5-HT2 receptor sequence.
 Query Match 5.9%; Score 71; DB 5; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1091
 ID ABB81765 standard; protein; 471 AA.
 DE Human 5-HT2A receptor protein SEQ ID NO:12.
 PN WO200261087-A2.
 PD 08-AUG-2002.
 PA (LIFE-) LIFESPAN BIOSCIENCES INC.
 DE Human 5-HT2A receptor protein SEQ ID NO:12.
 Query Match 5.9%; Score 71; DB 6; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1092
 ID ADC22641 standard; protein; 471 AA.
 DE Human G protein-coupled receptor (GPCR) polypeptide #32.
 PN US6555339-B1.
 PD 29-APR-2003.
 PA (AREN-) ARENA PHARM INC.
 DE Human G protein-coupled receptor (GPCR) polypeptide #72.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1093
 ID ADC22747 standard; protein; 471 AA.
 DE Human G protein-coupled receptor (GPCR) polypeptide #72.
 PN US6555339-B1.
 PD 29-APR-2003.
 PA (AREN-) ARENA PHARM INC.
 DE Human G protein-coupled receptor (GPCR) polypeptide #72.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1094

ID ADE5844 standard; protein; 471 AA.
 DE Human serotonin 2A receptor.
 PN US2003170723-A1.
 PD 11-SEP-2003.
 PA (SATO/) SATO T.
 DE Human serotonin 2A receptor.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1095
 ID ADH14220 standard; protein; 471 AA.
 DE Mutated human serotonin 5HT_2A.
 PN US2003105292-A1.
 PD 05-JUN-2003.
 PA (LIAW/) LIAW C W.
 PA (BEHA/) BEHAN D P.
 PA (CHAL/) CHALMERS D T.
 DE Human serotonin 5HT_2A.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1096
 ID ADH14114 standard; protein; 471 AA.
 DE Human serotonin 5HT_2A.
 PN US2003105292-A1.
 PD 05-JUN-2003.
 PA (LIAW/) LIAW C W.
 PA (BEHA/) BEHAN D P.
 PA (CHAL/) CHALMERS D T.
 DE Human serotonin 5HT_2A.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1097
 ID ADL90125 standard; protein; 471 AA.
 DE Human serotonin receptor 5HT2A.
 PN US2003167476-A1.
 PD 04-SEP-2003.
 PA (CONK/) CONKLIN B R.
 DE Human serotonin receptor 5HT2A.
 Query Match 5.9%; Score 71; DB 7; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1098
 ID ADO29506 standard; protein; 471 AA.
 DE Human GPCR HTR2A, SEQ ID NO:608.
 PN WO2004040000-A2.
 PD 13-MAY-2004.
 PA (PRIM-) PRIMM INC.
 DE Human GPCR HTR2A, SEQ ID NO:608.
 Query Match 5.9%; Score 71; DB 8; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1099
 ID ADO39800 standard; protein; 471 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1463.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1463.
 Query Match 5.9%; Score 71; DB 8; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1100
 ID ADO39799 standard; protein; 471 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1462.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1462.
 Query Match 5.9%; Score 71; DB 8; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1101
 ID ADO39798 standard; protein; 471 AA.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1461.
 PN WO2004058052-A2.
 PD 15-JUL-2004.
 PA (APPL-) APPLERA CORP.
 DE Human myocardial infarction-associated gene derived protein, SEQ ID 1461.
 Query Match 5.9%; Score 71; DB 8; Length 471;
 Best Local Similarity 23.7%; Pred. No. 60;
 RESULT 1102
 ID AAY01626 standard; protein; 478 AA.
 DE Amino acid sequence of the human 5-HT2 receptor.
 PN US5885785-A.
 PD 23-MAR-1999.
 PA (SYNA-) SYNAPTIC PHARM CORP.

Query Match 5.9%; Score 71; DB 2; Length 478;
Best Local Similarity 23.7%; Pred. No. 61;
RESULT 1103
ID ABG70577 standard; protein; 480 AA.
DE Human serotonin (5-HT2) receptor.
PN US2002098548-A1.
PD 25-JUL-2002.
PA (SYNA-) SYNAPTIC PHARM CORP.
Query Match 5.9%; Score 71; DB 5; Length 480;
Best Local Similarity 23.7%; Pred. No. 62;
RESULT 1104
ID AAM70440 standard; protein; 493 AA.
DE Photorehabus luminescens protein sequence #3537.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
PA (CNRS) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 71; DB 6; Length 493;
Best Local Similarity 23.5%; Pred. No. 64;
RESULT 1105
ID ADE56383 standard; protein; 545 AA.
DE Rat Protein O70536, SEQ ID NO 2235.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 7; Length 545;
Best Local Similarity 22.0%; Pred. No. 73;
RESULT 1106
ID ADD48660 standard; protein; 545 AA.
DE Rat Protein BAA25372, SEQ ID NO 14366.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 7; Length 545;
Best Local Similarity 22.0%; Pred. No. 73;
RESULT 1107
ID ADS43584 standard; protein; 546 AA.
DE Bacterial polypeptide #22014.
PN US200233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 5.9%; Score 71; DB 8; Length 546;
Best Local Similarity 26.2%; Pred. No. 74;
RESULT 1108
ID AAJ26399 standard; protein; 559 AA.
DE Aspergillus fumigatus essential gene protein #1057.
PN WO200286090-A2.
PD 31-OCT-2002.
PA (ELIT) ELITTA PHARM INC.
Query Match 5.9%; Score 71; DB 6; Length 559;
Best Local Similarity 23.1%; Pred. No. 76;
RESULT 1109
ID ABB35686 standard; protein; 563 AA.
DE Fungal Zbc protein sequence #112.
PN WO200224865-A2.
PD 28-MAR-2002.
PA (MICR-) MICROBIA INC.
Query Match 5.9%; Score 71; DB 5; Length 563;
Best Local Similarity 19.1%; Pred. No. 77;
RESULT 1110
ID AAB20578 standard; protein; 564 AA.
DE Mouse OCTN3 protein SEQ ID NO:1.
PN WO2000046368-A1.
PD 10-AUG-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.9%; Score 71; DB 3; Length 564;
Best Local Similarity 21.4%; Pred. No. 77;

RESULT 1111
ID ADQ96374 standard; protein; 631 AA.
DE T cell activation associated protein #76.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 5.9%; Score 71; DB 8; Length 631;
Best Local Similarity 21.3%; Pred. No. 90;
RESULT 1112
ID ADQ96376 standard; protein; 631 AA.
DE T cell activation associated protein #277.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 5.9%; Score 71; DB 8; Length 631;
Best Local Similarity 21.3%; Pred. No. 90;
RESULT 1113
ID ABB91532 standard; protein; 676 AA.
DE Herbicidally active polypeptide SEQ ID NO 743.
PN WO200210210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 5; Length 676;
Best Local Similarity 22.3%; Pred. No. 99;
RESULT 1114
ID AAE21800 standard; protein; 727 AA.
DE Human HIPHUM 0000029 protein.
PN GB2365432-A.
PD 20-FEB-2002.
PA (GLAX) GLAXO GROUP LTD.
Query Match 5.9%; Score 71; DB 5; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1115
ID ABB54636 standard; protein; 727 AA.
DE Human NOVX polypeptide #95.
PN WO200281498-A2.
PD 17-OCT-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.9%; Score 71; DB 6; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1116
ID ADH76500 standard; protein; 727 AA.
DE 727 amino acid human neurotransmitter transporter protein.
PN US200321974-A1.
PD 27-NOV-2003.
PA (SHAR) SHARMA R.
PA (RAMA) RAMANATHAN C S.
PA (WEST) WESTPHAL R.
PA (FEDE) FEDER J N.
PA (LEEL) LEE L M.
Query Match 5.9%; Score 71; DB 8; Length 727;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1117
ID AAB62929 standard; protein; 744 AA.
DE Human neurotransmitter transporter.
PN WO2003055947-A1.
PD 24-JUL-2003.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 71; DB 7; Length 744;
Best Local Similarity 24.3%; Pred. No. 1.1e+02;
RESULT 1118
ID ABB60052 standard; protein; 792 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6948.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PBKE) PE CORP NY.
Query Match 5.9%; Score 71; DB 4; Length 792;
Best Local Similarity 17.7%; Pred. No. 1.2e+02;
RESULT 1119
ID AAR30616 standard; protein; 3010 AA.
DE Polypeptide coded by Korean HCV full cDNA sequence LBCL.
PN BF521518-A2.
PD 07-JAN-1993.

PA (LUCK-) LUCKY LTD.
 Query Match 5.9%; Score 71; DB 2; Length 3010;
 Best Local Similarity 26.9%; Pred. No. 7.8e+02;
 RESULT 1120
 ID AAR53417 standard; protein; 3010 AA.
 DE Blood transmissible NANBHV protein.
 PN JP6105690-A.
 PD 19-APR-1994.
 PA (KAEN/) KAENNO K.
 Query Match 5.9%; Score 71; DB 2; Length 3010;
 Best Local Similarity 26.9%; Pred. No. 7.8e+02;
 RESULT 1121
 ID ABR83573 standard; protein; 202 AA.
 DE BcrC amino acid sequence SEQ ID NO:40.
 PN WO2003057708-A2.
 PD 17-JUL-2003.
 PA (UYNE-) UNIV NEWCASTLE VENTURES LTD.
 Query Match 5.9%; Score 70.5; DB 6; Length 202;
 Best Local Similarity 26.5%; Pred. No. 21;
 RESULT 1122
 ID AAU01287 standard; protein; 218 AA.
 DE Brassica napus fatty acid desaturase, Fad3C, partial sequence.
 PN WO200125453-A2.
 PD 12-APR-2001.
 PA (MIAC-) CANADA MIN AGRIC & AGRI-FOOD CANADA.
 Query Match 5.9%; Score 70.5; DB 4; Length 218;
 Best Local Similarity 29.3%; Pred. No. 24;
 RESULT 1123
 ID AAU97208 standard; protein; 228 AA.
 DE Portion of a wheat sugar transport protein encoded by wreln.pk0006.b4.
 PN US6383776-B1.
 PD 07-MAY-2002.
 PA (DUPO-) DU FONT DE NEMOURS & CO E I.
 Query Match 5.9%; Score 70.5; DB 5; Length 228;
 Best Local Similarity 21.6%; Pred. No. 25;
 RESULT 1124
 ID ABU08333 standard; protein; 228 AA.
 DE Wheat sugar transport protein #3.
 PN US2002178466-A1.
 PD 28-NOV-2002.
 PA (ALLE/) ALLEN S M.
 PA (HITZ/) HITZ W D.
 PA (KINN/) KINNEY A J.
 PA (TING/) TINGEY S V.
 Query Match 5.9%; Score 70.5; DB 6; Length 228;
 Best Local Similarity 21.6%; Pred. No. 25;
 RESULT 1125
 ID ADG47920 standard; protein; 228 AA.
 DE Wheat Arabidopsis-like sugar transport protein #3.
 PN US2002199217-A1.
 PD 26-DEC-2002.
 PA (HELE/) HELENTARIS T G.
 Query Match 5.9%; Score 70.5; DB 8; Length 228;
 Best Local Similarity 21.6%; Pred. No. 25;
 RESULT 1126
 ID ABU17430 standard; protein; 275 AA.
 DE Protein encoded by prokaryotic essential gene #2957.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.9%; Score 70.5; DB 6; Length 275;
 Best Local Similarity 22.8%; Pred. No. 33;
 RESULT 1127
 ID ABB55033 standard; protein; 285 AA.
 DE Lactococcus lactis protein ma1G.
 PN FR2807446-A1.
 PD 12-OCT-2001.
 PA (INRG-) INRA INST NAT RECH AGRONOMICUE.
 Query Match 5.9%; Score 70.5; DB 5; Length 285;
 Best Local Similarity 26.1%; Pred. No. 34;
 RESULT 1128
 ID ABB05467 standard; protein; 291 AA.
 DE Cortisol versicolor aldo/ketoreductase protein SEQ ID NO:2.

PN JP2001321171-A.
 PD 20-NOV-2001.
 PA (WARI/) WARIISHI H.
 PA (KUBI/) KUBOTA CORP.
 Query Match 5.9%; Score 70.5; DB 5; Length 291;
 Best Local Similarity 29.4%; Pred. No. 35;
 RESULT 1129
 ID ADA35787 standard; protein; 297 AA.
 DE Acinetobacter baumannii protein #2948.
 PN US6562958-B1.
 PD 13-MAY-2003.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 70.5; DB 6; Length 297;
 Best Local Similarity 24.1%; Pred. No. 36;
 RESULT 1130
 ID AAM70358 standard; protein; 321 AA.
 DE Photorehabdus luminescens protein sequence #3455.
 PN WO200294867-A2.
 PD 28-NOV-2002.
 PA (INSP-) INST PASTEUR.
 PA (CNRS-) CNRS CENT NAT RECH SCI.
 Query Match 5.9%; Score 70.5; DB 6; Length 321;
 Best Local Similarity 19.2%; Pred. No. 40;
 RESULT 1131
 ID ADH22355 standard; protein; 330 AA.
 DE Human receptor & membrane associated protein (REMAP) SeqIDS.
 PN WO2003104395-A2.
 PD 18-DEC-2003.
 PA (INCY-) INCYTE CORP.
 Query Match 5.9%; Score 70.5; DB 8; Length 330;
 Best Local Similarity 24.2%; Pred. No. 42;
 RESULT 1132
 ID ADK68232 standard; protein; 343 AA.
 DE Novel NOVX protein #79.
 PN WO2003085124-A2.
 PD 16-OCT-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.9%; Score 70.5; DB 7; Length 343;
 Best Local Similarity 30.0%; Pred. No. 44;
 RESULT 1133
 ID ADH72226 standard; protein; 343 AA.
 DE Human protein of the invention NOV55a SEQ ID NO:1122.
 PN WO2003102155-A2.
 PD 11-DEC-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match 5.9%; Score 70.5; DB 8; Length 343;
 Best Local Similarity 30.0%; Pred. No. 44;
 RESULT 1134
 ID ADR49221 standard; protein; 343 AA.
 DE Human NOV10a protein.
 PN US2004162236-A1.
 PD 19-AUG-2004.
 PA (ALSO/) ALSOBROOK J.
 PA (BENT/) BENTO P.
 PA (BOLD/) BOLDG F.
 PA (BURG/) BURGESS C.
 PA (CASM/) CASMAN S.
 PA (BOKO/) BOKOR J C.
 PA (EDIN/) EDINGER S R.
 PA (ELLE/) ELLERMAN K.
 PA (FERN/) FERNANDES E.
 PA (GERL/) GERLACH V.
 PA (GROS/) GROSSE W.
 PA (GUNT/) GUNTHER E.
 PA (GUSE/) GUSEV V.
 PA (HEYE/) HEYES M.
 PA (LEPL/) LEPLLEY D.
 PA (LIIL/) LI L.
 PA (MACD/) MACDOUGALL J R.
 PA (MALI/) MALYANKAR U M.
 PA (MILT/) MILLET I.
 PA (PATY/) PATYRAJAN M.
 PA (PEYM/) PEYMAN J A.

PA (RAST/) RASTELLI L.
PA (RIEG/) RIEGER D.
PA (SHEN/) SHENY S.
PA (SHIM/) SHIMKETS R.
PA (SMIT/) SMITHSON G.
PA (STON/) STONE D.
PA (VERN/) VERNET C.
PA (VOSS/) VOSS E.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 343;
Pred. No. 44;
RESULT 1135
ID ADR40543 standard; protein; 363 AA.
DE Ovine melatonin receptor O4608 protein.
PN US2004161823-A1.
PD 19-AUG-2004.
PA (PEDE/) FEDER J N.
PA (MINT/) MINTIER G.
PA (RAMA/) RAMANATHAN C S.
PA (HAMK/) HAMKEN D R.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 363;
Pred. No. 48;
RESULT 1136
ID AAR69518 standard; protein; 365 AA.
DE Prostaglandin-EP3-9 receptor.
PN WO9500552-A1.
PD 05-JAN-1995.
PA (MERI/) MERCK FROST CANADA INC.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 2; Length 365;
Pred. No. 48;
RESULT 1137
ID AAB38521 standard; protein; 365 AA.
DE Human PTGER3 protein isoform, EP3b.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 7; Length 365;
Pred. No. 48;
RESULT 1138
ID ADI35077 standard; protein; 365 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #9.
PN US2003243393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 365;
Pred. No. 48;
RESULT 1139
ID ADL15869 standard; protein; 365 AA.
DE Human prostaglandin EP3 receptor #3.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR/) ALLERGAN INC.
PA (UYAR/) UNIV ARIZONA.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 365;
Pred. No. 48;
RESULT 1140
ID ADR67864 standard; protein; 365 AA.
DE Prostaglandin E2 EP3 III.
PN WO2004074830-A2.
PD 02-SEP-2004.
PA (FARB/) BAYER HEALTHCARE AG.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 365;
Pred. No. 48;
RESULT 1141
ID ADS21429 standard; protein; 366 AA.
DE Bacterial polypeptide #10462.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match
5.9%; Score 70.5; DB 8; Length 366;
Pred. No. 48;

Best Local Similarity 21.2%; Pred. No. 48;
RESULT 1142
ID ADF04358 standard; protein; 367 AA.
DE Bacterial polypeptide #471.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 7; Length 367;
Pred. No. 49;
RESULT 1143
ID AAE38520 standard; protein; 374 AA.
DE Human PTGER3 protein isoform, EP3d.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 7; Length 374;
Pred. No. 50;
RESULT 1144
ID ADI35075 standard; protein; 374 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #8.
PN US2003243393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 374;
Pred. No. 50;
RESULT 1145
ID AAR48711 standard; protein; 379 AA.
DE G-protein coupled rat serotonin 2 receptor protein.
PN WO9405695-A1.
PD 17-MAR-1994.
PA (UYNY/) UNIV NEW YORK STATE.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 2; Length 379;
Pred. No. 51;
RESULT 1146
ID AAM02683 standard; peptide; 379 AA.
DE G-protein coupled rat serotonin 2 receptor.
PN US5508384-A.
PD 16-APR-1996.
PA (UYNY/) UNIV NEW YORK STATE.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 2; Length 379;
Pred. No. 51;
RESULT 1147
ID AAR69517 standard; protein; 388 AA.
DE Prostaglandin-EP3-21 receptor.
PN WO9500552-A1.
PD 05-JAN-1995.
PA (MERI/) MERCK FROST CANADA INC.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 2; Length 388;
Pred. No. 52;
RESULT 1148
ID AAE38513 standard; protein; 388 AA.
DE Human PTGER3 protein isoform, EP3c.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 7; Length 388;
Pred. No. 52;
RESULT 1149
ID ADI35061 standard; protein; 388 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #1.
PN US2003243393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match
Best Local Similarity 5.9%; Score 70.5; DB 8; Length 388;
Pred. No. 52;
RESULT 1150
ID ADL15887 standard; protein; 388 AA.
DE Human prostaglandin EP3 receptor #2.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR/) ALLERGAN INC.
PA (UYAR/) UNIV ARIZONA.
Query Match
5.9%; Score 70.5; DB 8; Length 388;
Pred. No. 52;

Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1151
ID AD813753 standard; protein; 388 AA.
DE Human prostaglandin E2 EP3 II polypeptide.
PN WO2004075813-A2.
PD 10-SEP-2004.
PA (PARB) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 8; Length 388;
Best Local Similarity 24.2%; Pred. No. 52;
RESULT 1152
ID AAR69516 standard; protein; 390 AA.
DE Prostaglandin-EP3-alpha receptor.
PN WO9500552-A1.
PD 05-JAN-1995.
PA (MERI) MERCK FROSST CANADA INC.
Query Match 5.9%; Score 70.5; DB 2; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1153
ID AAB38516 standard; protein; 390 AA.
DE Human PTGER3 protein isoform, EP3a1.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1154
ID AAB38517 standard; protein; 390 AA.
DE Human PTGER3 protein isoform, EP3a2.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1155
ID AD135067 standard; protein; 390 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #4.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1156
ID AD135069 standard; protein; 390 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #5.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1157
ID AD135698 standard; protein; 390 AA.
DE Human prostaglandin EP3 receptor #4.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1158
ID AD15885 standard; protein; 390 AA.
DE Human prostaglandin EP3 receptor #1.
PN US6670134-B1.
PD 30-DEC-2003.
PA (ALLR) ALLERGAN INC.
PA (UYAR-) UNIV ARIZONA.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1159
ID ADR70434 standard; protein; 390 AA.
DE Human prostaglandin E2 EP3 protein.
PN WO2004074842-A2.
PD 02-SEP-2004.
PA (PARB) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1160
ID AD576168 standard; protein; 390 AA.
DE Prostaglandin E2 EP3 I.
PN WO2004075814-A2.
PD 10-SEP-2004.
PA (PARB) BAYER HEALTHCARE AG.
Query Match 5.9%; Score 70.5; DB 8; Length 390;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1161
ID AAM57411 standard; protein; 393 AA.
DE Human prostaglandin EP3-VI receptor.
PN JP10113185-A.
PD 06-MAY-1998.
PA (ONOX) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1162
ID AAB38519 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3e.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1163
ID AAB38523 standard; protein; 393 AA.
DE Human PTGER3 protein isoform, EP3-VI.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1164
ID AD135081 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #11.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1165
ID AD135073 standard; protein; 393 AA.
DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #7.
PN US2003224393-A1.
PD 04-DEC-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 8; Length 393;
Best Local Similarity 24.2%; Pred. No. 53;
RESULT 1166
ID AAM57410 standard; protein; 402 AA.
DE Human EP3-V receptor.
PN JP10113185-A.
PD 06-MAY-1998.
PA (ONOX) ONO PHARM CO LTD.
Query Match 5.9%; Score 70.5; DB 2; Length 402;
Best Local Similarity 24.2%; Pred. No. 55;
RESULT 1167
ID AAP81904 standard; protein; 402 AA.
DE Human prostaglandin E2 receptor EP3 protein SEQ ID NO:294.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 70.5; DB 6; Length 402;
Best Local Similarity 24.2%; Pred. No. 55;
RESULT 1168
ID AAB38522 standard; protein; 402 AA.
DE Human PTGER3 protein isoform, EP3-V.
PN WO2003064471-A2.
PD 07-AUG-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.9%; Score 70.5; DB 7; Length 402;

Best Local Similarity 24.2%; Pred. No. 55;
 RESULT 1169
 ID AD135079 standard; protein: 402 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #10.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 402;
 Best Local Similarity 24.2%; Pred. No. 55;
 RESULT 1170
 ID ADO5167 standard; protein: 402 AA.
 DE Protein #69 with increased gene expression in renal cell carcinoma.
 PN WO2004032842-A2.
 PD 22-APR-2004.
 PA (VAND-) VAN ANDEL INST.
 Query Match 5.9%; Score 70.5; DB 8; Length 402;
 Best Local Similarity 24.2%; Pred. No. 55;
 RESULT 1171
 ID ADO29620 standard; protein: 402 AA.
 DE Human GPCR PTGER3, SEQ ID NO:1722.
 PN WO2004040000-A2.
 PD 13-MAY-2004.
 PA (PRIM-) PRIMAL INC.
 Query Match 5.9%; Score 70.5; DB 8; Length 402;
 Best Local Similarity 24.2%; Pred. No. 55;
 RESULT 1172
 ID AAB38514 standard; protein: 407 AA.
 DE Human PTGER3 protein isoform, EP3g.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 407;
 Best Local Similarity 24.2%; Pred. No. 56;
 RESULT 1173
 ID AD135063 standard; protein: 407 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #2.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 407;
 Best Local Similarity 24.2%; Pred. No. 56;
 RESULT 1174
 ID AAB38518 standard; protein: 425 AA.
 DE Human PTGER3 protein isoform, EP3f.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 425;
 Best Local Similarity 24.2%; Pred. No. 59;
 RESULT 1175
 ID AD135071 standard; protein: 425 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #6.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 425;
 Best Local Similarity 24.2%; Pred. No. 59;
 RESULT 1176
 ID AAB38515 standard; protein: 433 AA.
 DE Human PTGER3 protein isoform, EP3h.
 PN WO2003064471-A2.
 PD 07-AUG-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 7; Length 433;
 Best Local Similarity 24.2%; Pred. No. 61;
 RESULT 1177
 ID AD135065 standard; protein: 433 AA.
 DE Human prostaglandin E receptor subtype EP3 (PTGER3) protein #3.
 PN US2003224393-A1.
 PD 04-DEC-2003.
 PA (DECO-) DECODE GENETICS EHF.
 Query Match 5.9%; Score 70.5; DB 8; Length 433;
 Best Local Similarity 24.2%; Pred. No. 61;

RESULT 1178
 ID AAW98431 standard; protein: 480 AA.
 DE H. pylori GHPD 446 protein.
 PN WO9843478-A1.
 PD 08-OCT-1998.
 PA (INMR-) MERIEUX ORAVAX PASTEUR MERIEUX SERUMS.
 PA (HUMA-) HUMAN GENOME SCI INC.
 Query Match 5.9%; Score 70.5; DB 2; Length 480;
 Best Local Similarity 23.1%; Pred. No. 70;
 RESULT 1179
 ID ABR40525 standard; protein: 499 AA.
 DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5370.
 PN US6380370-B1.
 PD 30-APR-2002.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.9%; Score 70.5; DB 5; Length 499;
 Best Local Similarity 20.5%; Pred. No. 74;
 RESULT 1180
 ID ADS06092 standard; protein: 499 AA.
 DE Staphylococcus epidermidis seqid 5387.
 PN US2004147734-A1.
 PD 29-JUL-2004.
 PA (DOUC-) DOUCETTE-STAMM L.
 PA (BUSH-) BUSH D.
 Query Match 5.9%; Score 70.5; DB 8; Length 499;
 Best Local Similarity 20.5%; Pred. No. 74;
 RESULT 1181
 ID ABU30473 standard; protein: 521 AA.
 DE Protein encoded by Prokaryotic essential gene #16000.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (BLIT-) BLITRA PHARM INC.
 Query Match 5.9%; Score 70.5; DB 6; Length 521;
 Best Local Similarity 23.7%; Pred. No. 79;
 RESULT 1182
 ID AAU97213 standard; protein: 539 AA.
 DE Wheat sugar transport protein encoded by wlk8.pk0001.all.
 PN US6383776-B1.
 PD 07-MAY-2002.
 PA (DUPO-) DU PONT DE NEMOURS & CO E I.
 Query Match 5.9%; Score 70.5; DB 5; Length 539;
 Best Local Similarity 26.0%; Pred. No. 83;
 RESULT 1183
 ID ABU08338 standard; protein: 539 AA.
 DE Wheat sugar transport protein #4.
 PN US2002178468-A1.
 PD 28-NOV-2002.
 PA (ALBE/) ALLEN S M.
 PA (HITZ/) HITZ W D.
 PA (KINN/) KINNEY A J.
 PA (TING/) TINGEY S V.
 Query Match 5.9%; Score 70.5; DB 6; Length 539;
 Best Local Similarity 26.0%; Pred. No. 83;
 RESULT 1184
 ID ADG47930 standard; protein: 539 AA.
 DE Wheat Beta-vulgaris-like sugar transport protein #1.
 PN US2002199217-A1.
 PD 26-DEC-2002.
 PA (HELE/) HELENTJARIS T G.
 Query Match 5.9%; Score 70.5; DB 8; Length 539;
 Best Local Similarity 26.0%; Pred. No. 83;
 RESULT 1185
 ID ABU27418 standard; protein: 548 AA.
 DE Protein encoded by Prokaryotic essential gene #12945.
 PN WO200277183-A2.
 PD 03-OCT-2002.
 PA (BLIT-) BLITRA PHARM INC.
 Query Match 5.9%; Score 70.5; DB 6; Length 548;
 Best Local Similarity 24.0%; Pred. No. 85;
 RESULT 1186
 ID ADN22789 standard; protein: 556 AA.
 DE Bacterial polypeptide #5442.
 PN US2003233675-A1.

PD 18-DEC-2003.
 PA (CAOV/) CAO Y.
 PA (HINK/) HINKLE G J.
 PA (SLAT/) SLATER S C.
 PA (CHEN/) CHEN X.
 PA (GOLD/) GOLDMAN B S.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 556;
 RESULT 1187
 ID ADD46023 standard; protein: 599 AA.
 DE Rat Protein P23978, SEQ ID NO 11695.
 PN W02003016475-A2.
 PD 27-FEB-2003.
 PA (GEHO) GEN HOSPITAL CORP.
 PA (PARB) BAYER AG.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 599;
 RESULT 1188
 ID AAM02687 standard; protein: 599 AA.
 DE Rattus norvegicus neuronal GABA transporter (GAT-1).
 PN U62003143729-A1.
 PD 31-JUL-2003.
 PA (SYNA-) SYNAPTIC PHARM CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 599;
 RESULT 1189
 ID AAM78767 standard; protein: 600 AA.
 DE Human protein SEQ ID NO 1429.
 PN W0200157190-A2.
 PD 09-AUG-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 4; Length 600;
 RESULT 1190
 ID ADJ64315 standard; protein: 662 AA.
 DE Cartilage differentiation inhibiting protein, SEQ ID 10.
 PN W02004013326-A1.
 PD 12-FEB-2004.
 PA (ASAH) ASAH KASEI KK.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 662;
 RESULT 1191
 ID ABB92892 standard; protein: 700 AA.
 DE Herbicidally active polypeptide SEQ ID NO 2103.
 PN W0200210210-A2.
 PD 07-FEB-2002.
 PA (PARB) BAYER AG.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 700;
 RESULT 1192
 ID AAB56721 standard; protein: 717 AA.
 DE Human prostate cancer antigen protein sequence SEQ ID NO:1299.
 PN W0200055174-A1.
 PD 21-SEP-2000.
 PA (HUMA-) HUMAN GENOME SCI INC.
 PA (ROSE/) ROSEN C A.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 717;
 RESULT 1193
 ID AOC47941 standard; protein: 740 AA.
 DE Arabidopsis thaliana-1like sugar transport protein #2.
 PN U62002199217-A1.
 PD 26-DEC-2002.
 PA (HELE/) HELENTARIS T G.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 740;
 RESULT 1194
 ID AAG39555 standard; protein: 766 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48959.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 766;
 RESULT 1195
 ID AAG39555 standard; protein: 815 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 815;
 RESULT 1196
 ID AAG39553 standard; protein: 927 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 927;
 RESULT 1197
 ID AEP73754 standard; protein: 1026 AA.
 DE Candida albicans essential protein SEQ ID NO 7591.
 PN W0200253728-A2.
 PD 11-JUL-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 1026;
 RESULT 1198
 ID AAM17057 standard; protein: 1027 AA.
 DE Candida albicans chitin synthase (CHS1).
 PN W09716540-A1.
 PD 09-MAY-1997.
 PA (CHEM-) CHEMGENICS PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 1027;
 RESULT 1199
 ID ADH22510 standard; protein: 1147 AA.
 DE Human transporter & ion channel (TRICH) protein SeqID8.
 PN W0200309344-A2.
 PD 13-NOV-2003.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 1147;
 RESULT 1200
 ID ADK18350 standard; protein: 1163 AA.
 DE Human NOVX protein #2.
 PN W02003057854-A2.
 PD 17-JUL-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 1163;
 RESULT 1201
 ID ADM29274 standard; protein: 1163 AA.
 DE Human novel protein NOV2b.
 PN W02003064628-A2.
 PD 07-AUG-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 1163;
 RESULT 1202
 ID AAM53863 standard; peptide: 1780 AA.
 DE Human gravin polypeptide.
 PN U65741890-A.
 PD 21-APR-1998.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 1780;
 RESULT 1203
 ID AAB15380 standard; protein: 1780 AA.
 DE Human gravin protein sequence.
 PN U66090929-A.
 PD 18-JUL-2000.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 1780;
 RESULT 1204
 ID AAO17365 standard; protein: 1781 AA.
 DE Human gravin.

RESULT 1195
 ID AAG39555 standard; protein: 815 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48958.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 815;
 RESULT 1196
 ID AAG39553 standard; protein: 927 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 48957.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 927;
 RESULT 1197
 ID AEP73754 standard; protein: 1026 AA.
 DE Candida albicans essential protein SEQ ID NO 7591.
 PN W0200253728-A2.
 PD 11-JUL-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 1026;
 RESULT 1198
 ID AAM17057 standard; protein: 1027 AA.
 DE Candida albicans chitin synthase (CHS1).
 PN W09716540-A1.
 PD 09-MAY-1997.
 PA (CHEM-) CHEMGENICS PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 1027;
 RESULT 1199
 ID ADH22510 standard; protein: 1147 AA.
 DE Human transporter & ion channel (TRICH) protein SeqID8.
 PN W0200309344-A2.
 PD 13-NOV-2003.
 PA (INCY-) INCYTE CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 8; Length 1147;
 RESULT 1200
 ID ADK18350 standard; protein: 1163 AA.
 DE Human NOVX protein #2.
 PN W02003057854-A2.
 PD 17-JUL-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 1163;
 RESULT 1201
 ID ADM29274 standard; protein: 1163 AA.
 DE Human novel protein NOV2b.
 PN W02003064628-A2.
 PD 07-AUG-2003.
 PA (CURA-) CURAGEN CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 7; Length 1163;
 RESULT 1202
 ID AAM53863 standard; peptide: 1780 AA.
 DE Human gravin polypeptide.
 PN U65741890-A.
 PD 21-APR-1998.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 2; Length 1780;
 RESULT 1203
 ID AAB15380 standard; protein: 1780 AA.
 DE Human gravin protein sequence.
 PN U66090929-A.
 PD 18-JUL-2000.
 PA (UYOR-) UNIV OREGON HEALTH SCI.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 3; Length 1780;
 RESULT 1204
 ID AAO17365 standard; protein: 1781 AA.
 DE Human gravin.

PN EPI191107-A2.
 PD 27-MAR-2002.
 PA (SCHD) SCHERING AG.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 1781;
 RESULT 1203
 ID AB003477 standard; protein; 1781 AA.
 DE Angiogenesis-associated human protein sequence #22.
 PN W0200279492-A2.
 PD 10-OCT-2002.
 PA (BOSR-) BOS BIOTECHNOLOGY INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 6; Length 1781;
 RESULT 1206
 ID ABB97448 standard; protein; 1783 AA.
 DE Novel human protein SEQ ID NO: 716.
 PN W020022660-A2.
 PD 21-MAR-2002.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 5; Length 1783;
 RESULT 1207
 ID ABG21018 standard; protein; 1795 AA.
 DE Novel human diagnostic protein #21009.
 PN W0200175067-A2.
 PD 11-OCT-2001.
 PA (HYSE-) HYSEQ INC.
 Query Match
 Best Local Similarity 5.9%; Score 70.5; DB 4; Length 1795;
 RESULT 1208
 ID AAG34442 standard; protein; 185 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 41631.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 3; Length 185;
 RESULT 1209
 ID AAG34441 standard; protein; 189 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 41630.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 3; Length 189;
 RESULT 1210
 ID AAW44944 standard; protein; 225 AA.
 DE Avian infectious bronchitis virus glycoprotein M.
 PN FR2751225-A1.
 PD 23-JAN-1998.
 PA (INMR) RHONE MERIEUX SA.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 2; Length 225;
 RESULT 1211
 ID ADB09893 standard; protein; 226 AA.
 DE Allostercoccus oitidis antigenic protein SEQ ID NO:3730.
 PN W02003048304-A2.
 PD 12-JUN-2003.
 PA (AMHP) WYETH HOLDINGS CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 6; Length 226;
 RESULT 1212
 ID AAG34240 standard; protein; 235 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 41629.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 3; Length 235;
 RESULT 1213
 ID ABB69790 standard; protein; 256 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 36162.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 4; Length 256;

Best Local Similarity 20.2%; Pred. No. 34;
 RESULT 1214
 ID ADS96502 standard; protein; 256 AA.
 DE Drosophila melanogaster protein, SEQ ID 123.
 PN W02004039999-A2.
 PD 13-MAY-2004.
 PA (SYGN) SYNGENTA PARTICIPATIONS AG.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 8; Length 256;
 RESULT 1215
 ID ADP05703 standard; protein; 256 AA.
 DE Haemophilus influenzae (NTHI) protein - SEQ ID 739.
 PN W02004078949-A2.
 PD 16-SEP-2004.
 PA (CHIL-) CHILDRENS HOSPITAL INC.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 8; Length 256;
 RESULT 1216
 ID AAG53762 standard; protein; 274 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 68478.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 3; Length 274;
 RESULT 1217
 ID AAG53761 standard; protein; 287 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 68477.
 PN EPI033405-A2.
 PD 06-SEP-2000.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 3; Length 287;
 RESULT 1218
 ID ABU5677 standard; protein; 292 AA.
 DE Protein encoded by Prokaryotic essential gene #21204.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELITR-) ELITRA PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 6; Length 292;
 RESULT 1219
 ID ADK4848 standard; protein; 307 AA.
 DE Streptococcus pneumoniae protein, Seq ID No 5003.
 PN US669703-B1.
 PD 02-MAR-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 8; Length 307;
 RESULT 1220
 ID AAR72985 standard; protein; 333 AA.
 DE Epsilon opioid receptor.
 PN W09512670-A1.
 PD 11-MAY-1995.
 PA (ALCO-) ALCOHOLISM & DRUG ADDICTION RES FOUND.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 2; Length 333;
 RESULT 1221
 ID AAY90613 standard; protein; 333 AA.
 DE Human G protein-coupled receptor GPR8.
 PN W0200022129-A1.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 3; Length 333;
 RESULT 1222
 ID AAY90647 standard; protein; 333 AA.
 DE Human mutant G protein-coupled receptor GPR8 (T259K).
 PN W0200022129-A1.
 PD 20-APR-2000.
 PA (AREN-) ARENA PHARM INC.
 Query Match
 Best Local Similarity 5.9%; Score 70; DB 3; Length 333;
 RESULT 1223
 ID AAU01297 standard; protein; 333 AA.

DE Human G-protein receptor 8, GPR 8, mutant N127A.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M.
Query Match 5.9%; Score 70; DB 4; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1224
ID AAU01295 standard; protein; 333 AA.
DE Human G-protein receptor 8, GPR 8.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M.
Query Match 5.9%; Score 70; DB 4; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1225
ID AAU01298 standard; protein; 333 AA.
DE Human G-protein receptor 8, GPR 8, mutant T259B.
PN WO200127632-A2.
PD 19-APR-2001.
PA (CAMP-) CAMBRIDGE DRUG DISCOVERY LTD.
PA (WILL/) WILLIAMS K M.
Query Match 5.9%; Score 70; DB 4; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1226
ID ABB84683 standard; protein; 333 AA.
DE Human GPR8-11 ligand related protein #1.
PN WO200198494-A1.
PD 27-DEC-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 5; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1227
ID ABB84723 standard; protein; 333 AA.
DE Human GPR8-11 ligand related protein #3.
PN WO200198494-A1.
PD 27-DEC-2001.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 5; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1228
ID ABG65918 standard; protein; 333 AA.
DE G-protein-coupled receptor related peptide #6.
PN WO200244368-A1.
PD 06-JUN-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 5; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1229
ID ABU61448 standard; protein; 333 AA.
DE Screening method related protein #1.
PN WO200293161-A1.
PD 21-NOV-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1230
ID ABJ37874 standard; protein; 333 AA.
DE GPR7 11 ligand related human protein SEQ ID NO 84.
PN WO2002102847-A1.
PD 27-DEC-2002.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1231
ID ABB81897 standard; protein; 333 AA.
DE Human G-protein-coupled receptor GPR8 protein SEQ ID NO:279.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.9%; Score 70; DB 6; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;

RESULT 1232
ID ABR57245 standard; protein; 333 AA.
DE Human GPR8 protein SEQ ID NO:84.
PN WO2003045994-A1.
PD 05-JUN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1233
ID ADC22691 standard; protein; 333 AA.
DE Human G-protein-coupled receptor (GPCR) polypeptide #44.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1234
ID ADC22535 standard; protein; 333 AA.
DE Human G-protein-coupled receptor (GPCR) polypeptide #5.
PN US6555339-B1.
PD 29-APR-2003.
PA (AREN-) ARENA PHARM INC.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1235
ID ADC51793 standard; protein; 333 AA.
DE Human GPR8, SEQ ID 4.
PN WO2003057236-A1.
PD 17-JUL-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1236
ID ABR61545 standard; protein; 333 AA.
DE Human GPR8 receptor polypeptide.
PN WO2003081234-A2.
PD 02-OCT-2003.
PA (FARB) BAYER AG.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1237
ID ADG41976 standard; protein; 333 AA.
DE Human GPR8 polypeptide.
PN JP200309867-A.
PD 14-JAN-2003.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1238
ID ADH14008 standard; protein; 333 AA.
DE Human GPR8.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAM/) LIAM C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1239
ID ADH14164 standard; protein; 333 AA.
DE Mutated human GPR8.
PN US2003105292-A1.
PD 05-JUN-2003.
PA (LIAM/) LIAM C W.
PA (BEHA/) BEHAN D P.
PA (CHAL/) CHALMERS D T.
Query Match 5.9%; Score 70; DB 7; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1240
ID ADG12852 standard; protein; 333 AA.
DE Human wild-type hGPR8 amino acid sequence SEQ ID NO:75.
PN WO2003097795-A2.
PD 27-NOV-2003.

PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1241
ID ADO29700 standard; protein; 333 AA.
DE Human GPCR GPR8, SEQ ID NO:802.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1242
ID ADO31044 standard; protein; 333 AA.
DE Human GPCR GPR8, SEQ ID NO:73.
PN WO2004041301-A1.
PD 21-MAY-2004.
PA (TAKE-) TAKEEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1243
ID ADO19919 standard; protein; 333 AA.
DE Human soft tissue sarcoma-upregulated protein - SEQ ID 2738.
PN WO2004048938-A2.
PD 10-JUN-2004.
PA (PROT-) PROTEIN DESIGN LABS INC.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1244
ID ADS14162 standard; protein; 333 AA.
DE Human GPR8 ligand protein Seg1d 73.
PN WO2004080485-A1.
PD 23-SEP-2004.
PA (TAKE-) TAKEEDA CHEM IND LTD.
Query Match 5.9%; Score 70; DB 8; Length 333;
Best Local Similarity 23.6%; Pred. No. 49;
RESULT 1245
ID ADO12854 standard; protein; 347 AA.
DE Human HA tagged wild-type hGPR8 amino acid sequence SEQ ID NO:77.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 347;
Best Local Similarity 23.6%; Pred. No. 51;
RESULT 1246
ID ABG30839 standard; protein; 364 AA.
DE Human calcium channel protein.
PN WO200252003-A2.
PD 04-JUL-2002.
PA (PARB-) BAYER AG.
Query Match 5.9%; Score 70; DB 5; Length 364;
Best Local Similarity 25.0%; Pred. No. 55;
RESULT 1247
ID ADG12856 standard; protein; 364 AA.
DE Human hGPR8-enhanced receptor amino acid sequence SEQ ID NO:79.
PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 55;
RESULT 1248
ID ADO28778 standard; protein; 364 AA.
DE Human GPR8-enhanced receptor.
PN US2004091946-A1.
PD 13-MAY-2004.
PA (OAKL/) OAKLEY R H.
PA (BARA/) BARAK L S.
PA (LAPO/) LAPORTE S A.
PA (CARO/) CARON M G.
Query Match 5.9%; Score 70; DB 8; Length 364;
Best Local Similarity 23.6%; Pred. No. 55;
RESULT 1249
ID ADO12858 standard; protein; 378 AA.
DE HA tagged hGPR8-enhanced receptor amino acid sequence SEQ ID NO:81.

PN WO2003097795-A2.
PD 27-NOV-2003.
PA (NORA-) NORAK BIOSCI INC.
Query Match 5.9%; Score 70; DB 8; Length 378;
Best Local Similarity 23.6%; Pred. No. 58;
RESULT 1250
ID ADN49121 standard; protein; 388 AA.
DE Mouse oxytocin receptor protein.
PN US2004086881-A1.
PD 06-MAY-2004.
PA (RAMA/) RAMANATHAN C S.
PA (GOPA/) GOPAL S.
PA (MINT/) MINTIER G A.
PA (FEDER/) FEDER J.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 60;
RESULT 1251
ID ADO29591 standard; protein; 388 AA.
DE Mouse GPCR OXTR, SEQ ID NO:693.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.9%; Score 70; DB 8; Length 388;
Best Local Similarity 24.8%; Pred. No. 60;
RESULT 1252
ID ADA54410 standard; protein; 399 AA.
DE Human protein, SEQ ID 1978.
PN EP1293569-A2.
PD 19-MAR-2003.
PA (HELT-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 62;
RESULT 1253
ID ABG99947 standard; protein; 399 AA.
DE Human novel polypeptide #60.
PN WO200274961-A1.
PD 26-SEP-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 6; Length 399;
Best Local Similarity 22.9%; Pred. No. 62;
RESULT 1254
ID ADO96947 standard; protein; 425 AA.
DE E. faecium protein sequence SEQ ID 6574.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 7; Length 425;
Best Local Similarity 25.9%; Pred. No. 68;
RESULT 1255
ID ADA34110 standard; protein; 470 AA.
DE Acinetobacter baumannii protein #1271.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 6; Length 470;
Best Local Similarity 23.5%; Pred. No. 78;
RESULT 1256
ID ABM67264 standard; protein; 474 AA.
DE Phototaxis luminescence protein sequence #361.
PN WO200294867-A2.
PD 28-NOV-2002.
PA (INSP-) INST PASTEUR.
PA (CNRS-) CNRS CENT NAT RECH SCI.
Query Match 5.9%; Score 70; DB 6; Length 474;
Best Local Similarity 22.9%; Pred. No. 79;
RESULT 1257
ID AAB16787 standard; protein; 475 AA.
DE Human transporter and ion channel-24 (TRICH-24) protein.
PN WO200192304-A2.
PD 06-DEC-2001.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 475;

Best Local Similarity 25.0%; Pred. No. 79;
RESULT 1258
ID ADAB9683 standard; protein; 506 AA.
DE Staphylococcus aureus antigenic protein #222.
PN W02003011899-A2.
PD 13-FEB-2003.
PA (UYSH-) UNIV SHEPFIELD.
PA (BIOS-) BIOSYNEXUS INC.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 87;
RESULT 1259
ID ABM72414 standard; protein; 506 AA.
DE Staphylococcus aureus protein #1654.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.9%; Score 70; DB 6; Length 506;
Best Local Similarity 20.1%; Pred. No. 87;
RESULT 1260
ID AAE21176 standard; protein; 540 AA.
DE Human TRICH-20 protein.
PN W0200212340-A2.
PD 14-FEB-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.9%; Score 70; DB 5; Length 540;
Best Local Similarity 25.0%; Pred. No. 95;
RESULT 1261
ID AAM39017 standard; protein; 552 AA.
DE Human polypeptide SEQ ID NO 2162.
PN W0200153312-A1.
PD 26-JUL-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.9%; Score 70; DB 4; Length 552;
Best Local Similarity 25.0%; Pred. No. 98;
RESULT 1262
ID ABU18262 standard; protein; 602 AA.
DE Protein encoded by Prokaryotic essential gene #3789.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 602;
Best Local Similarity 26.4%; Pred. No. 1.1e+02;
RESULT 1263
ID AAV33453 standard; protein; 637 AA.
DE Protein encoded by Prokaryotic essential gene #18980.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.9%; Score 70; DB 6; Length 637;
Best Local Similarity 23.1%; Pred. No. 1.2e+02;
RESULT 1264
ID AAY91335 standard; protein; 640 AA.
DE Group B streptococcus protein sequence SEQ ID NO:68.
PN W0200006736-A2.
PD 10-FEB-2000.
PA (MICR-) MICROBIAL TECHNIQS LTD.
Query Match 5.9%; Score 70; DB 3; Length 640;
Best Local Similarity 21.4%; Pred. No. 1.2e+02;
RESULT 1265
ID AAM83818 standard; protein; 695 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:4067.
PN W02004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.9%; Score 70; DB 8; Length 695;
Best Local Similarity 28.6%; Pred. No. 1.3e+02;
RESULT 1266
ID ADL04660 standard; protein; 767 AA.
DE M. catarrhalis protein #426.
PN U6673910-B1.
PD 06-JAN-2004.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.9%; Score 70; DB 8; Length 767;
Best Local Similarity 21.3%; Pred. No. 1.5e+02;
RESULT 1267
ID AAR53921 standard; protein; 980 AA.
DE HCV fusion protein corresp. to N-terminal of ORF.
PN JP06092996-A.
PD 05-APR-1994.
PA (SHIM/) SHIMOTOYA K.
Query Match 5.9%; Score 70; DB 2; Length 980;
Best Local Similarity 24.6%; Pred. No. 2.2e+02;
RESULT 1268
ID ADS24062 standard; protein; 1041 AA.
DE Bacterial polypeptide #13095.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.9%; Score 70; DB 8; Length 1041;
Best Local Similarity 23.4%; Pred. No. 2.4e+02;
RESULT 1269
ID ADP07803 standard; protein; 138 AA.
DE Human secreted protein, seq id 286.
PN W02004042000-A2.
PD 21-MAY-2004.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 8; Length 138;
Best Local Similarity 22.0%; Pred. No. 16;
RESULT 1270
ID ADA33664 standard; protein; 198 AA.
DE Actinobacter baumannii protein #825.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 198;
Best Local Similarity 23.3%; Pred. No. 27;
RESULT 1271
ID ADB09276 standard; protein; 201 AA.
DE Allicoccus citris antigenic protein SEQ ID NO:3216.
PN W02003048304-A2.
PD 12-JUN-2003.
PA (AMHP) MYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 201;
Best Local Similarity 26.0%; Pred. No. 28;
RESULT 1272
ID AAU29449 standard; protein; 210 AA.
DE Human G protein-coupled receptor (GPCR) polypeptide #70.
PN W0200168858-A2.
PD 20-SEP-2001.
PA (PHAA) PHARMACIA & UPJOHN CO.
Query Match 5.8%; Score 69.5; DB 4; Length 210;
Best Local Similarity 20.9%; Pred. No. 29;
RESULT 1273
ID ABG60737 standard; protein; 210 AA.
DE Novel G protein coupled receptor (NGCPR-x) #70.
PN US2002058306-A1.
PD 16-MAY-2002.
PA (VOGE/) VOGELI G.
Query Match 5.8%; Score 69.5; DB 5; Length 210;
Best Local Similarity 20.9%; Pred. No. 29;
RESULT 1274
ID AAV01288 standard; protein; 218 AA.
DE Braselica napus fatty acid desaturase, Fad3C, mutant partial sequence.
PN W0200125453-A2.
PD 12-APR-2001.
PA (MIAC) CANADA MIN AGRIC & AGRI-FOOD CANADA.
Query Match 5.8%; Score 69.5; DB 4; Length 218;
Best Local Similarity 29.3%; Pred. No. 31;
RESULT 1275
ID ADB09278 standard; protein; 247 AA.
DE Allicoccus citris antigenic protein SEQ ID NO:3218.
PN W02003048304-A2.

PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 247;
Best Local Similarity 26.0%; Pred. No. 37;
RESULT 1276
ID AAG66935 standard; protein; 253 AA.
DE Novel G-protein coupled receptor related protein #12.
PN W0200240539-A2.
PD 23-MAY-2002.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 253;
Best Local Similarity 24.2%; Pred. No. 38;
RESULT 1277
ID ABB62542 standard; protein; 261 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 14418.
PN W0200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69.5; DB 4; Length 261;
Best Local Similarity 27.7%; Pred. No. 40;
RESULT 1278
ID ABO80446 standard; protein; 270 AA.
DE Pseudomonas aeruginosa polypeptide #12621.
PN US6551795-B1.
PD 22-APR-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 270;
Best Local Similarity 22.1%; Pred. No. 42;
RESULT 1279
ID ADB86076 standard; protein; 296 AA.
DE Streptomyces hygroscopicus ABC transporter.
PN W02003082909-A1.
PD 09-OCT-2003.
PA (AMHP) WYETH.
Query Match 5.8%; Score 69.5; DB 7; Length 296;
Best Local Similarity 21.0%; Pred. No. 47;
RESULT 1280
ID AAG71524 standard; protein; 308 AA.
DE Human olfactory receptor polypeptide, SEQ ID NO: 1205.
PN W0200127158-A2.
PD 19-APR-2001.
PA (DIGI-) DIGISCENTS.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1281
ID ABB44525 standard; protein; 308 AA.
DE Human GPCR3 polypeptide SEQ ID NO 9.
PN W0200174904-A2.
PD 11-OCT-2001.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1282
ID AAU24742 standard; protein; 308 AA.
DE Human olfactory receptor AOLF242.
PN W0200168805-A2.
PD 20-SEP-2001.
PA (SENO-) SENOMYX INC.
Query Match 5.8%; Score 69.5; DB 4; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1283
ID ABP95703 standard; protein; 308 AA.
DE Human GPCR polypeptide SEQ ID NO 216.
PN W0200216548-A2.
PD 28-FEB-2002.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1284
ID AAU95729 standard; protein; 308 AA.
DE Human olfactory and pheromone G protein-coupled receptor #216.
PN W0200224726-A2.

PD 28-MAR-2002.
PA (CHEM-) CHEMCOM SA.
Query Match 5.8%; Score 69.5; DB 5; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1285
ID AAU85362 standard; protein; 308 AA.
DE G-coupled olfactory receptor #223.
PN W0200198526-A2.
PD 27-DEC-2001.
PA (SENO-) SENOMYX INC.
Query Match 5.8%; Score 69.5; DB 5; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1286
ID ADC86333 standard; protein; 308 AA.
DE Human GPCR protein SEQ ID NO:786.
PN EP1270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
Query Match 5.8%; Score 69.5; DB 7; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1287
ID ABW02126 standard; protein; 308 AA.
DE Human GPCR3 protein.
PN US2003195335-A1.
PD 16-OCT-2003.
PA (GROS/) GROSSE W M.
PA (SZEK/) SZEKERES E S.
PA (CASM/) CASMAN S.
PA (ALSO/) ALSOBROOK J P.
PA (BURG/) BURGESS C E.
PA (PADI/) PADIGARU M.
PA (TAYL/) TAYLOR S.
PA (TCHE/) TCHERNEV V T.
PA (SPYT/) SPYTEK K A.
PA (LILL/) LI L.
PA (SHEN/) SHENOY S.
PA (KEKU/) KEKUDA R.
PA (GANG/) GANGOLLI E A.
PA (STON/) STONE D J.
PA (SMIT/) SMITHSON G.
PA (MACD/) MACDOUGALL J R.
Query Match 5.8%; Score 69.5; DB 7; Length 308;
Best Local Similarity 20.9%; Pred. No. 50;
RESULT 1288
ID ABR01671 standard; protein; 316 AA.
DE Human G protein coupled receptor SEQ ID 202.
PN W02003000735-A2.
PD 03-JAN-2003.
PA (DECO-) DECODE GENETICS EHF.
Query Match 5.8%; Score 69.5; DB 6; Length 316;
Best Local Similarity 20.9%; Pred. No. 52;
RESULT 1289
ID AAY35360 standard; protein; 321 AA.
DE Chlamydia pneumoniae involved in the virulence process.
PN W09927105-A2.
PD 03-JUN-1999.
PA (GEST) GENSET.
Query Match 5.8%; Score 69.5; DB 2; Length 321;
Best Local Similarity 21.4%; Pred. No. 53;
RESULT 1290
ID ADC33485 standard; protein; 321 AA.
DE Yeast ARV1.
PN US6566512-B1.
PD 20-MAY-2003.
PA (UTCO) UNIV COLUMBIA NEW YORK.
Query Match 5.8%; Score 69.5; DB 7; Length 321;
Best Local Similarity 18.8%; Pred. No. 53;
RESULT 1291
ID ADE337749 standard; protein; 321 AA.
DE Yeast ARV1 (ARE-2 Required for viability).
PN US2003186879-A1.
PD 02-OCT-2003.

PA (UYCO) UNIV COLUMBIA NEW YORK.
 Query Match 5.8%; Score 69.5; DB 7; Length 321;
 Best Local Similarity 18.8%; Pred. No. 53;
 RESULT 1292
 ID AAV5139 standard; protein; 327 AA.
 DE Propionibacterium acnes immunogenic protein #14035.
 PN W0200181581-A2.
 PD 01-NOV-2001.
 PA (CORI-) CORIXA CORP.
 Query Match 5.8%; Score 69.5; DB 4; Length 327;
 Best Local Similarity 25.5%; Pred. No. 54;
 RESULT 1293
 ID ABM49658 standard; protein; 327 AA.
 DE Propionibacterium acnes predicted ORF-encoded polypeptide #14334.
 PN W02003033515-A1.
 PD 24-APR-2003.
 PA (CORI-) CORIXA CORP.
 Query Match 5.8%; Score 69.5; DB 6; Length 327;
 Best Local Similarity 25.5%; Pred. No. 54;
 RESULT 1294
 ID ADH10684 standard; protein; 354 AA.
 DE Rat Sprague-Dawley putative GCR polypeptide.
 PN W02003104484-A1.
 PD 18-DEC-2003.
 PA (META-) METABOLEX INC.
 Query Match 5.8%; Score 69.5; DB 8; Length 354;
 Best Local Similarity 22.0%; Pred. No. 61;
 RESULT 1295
 ID AAY05489 standard; protein; 382 AA.
 DE Human EDG-2 protein sequence.
 PN W09919513-A2.
 PD 22-APR-1999.
 PA (LXRB-) LXRB BIOTECHNOLOGY INC.
 Query Match 5.8%; Score 69.5; DB 2; Length 382;
 Best Local Similarity 20.2%; Pred. No. 67;
 RESULT 1296
 ID AAU00302 standard; protein; 382 AA.
 DE LPA receptor-related amino acid sequence #1.
 PN W0200112838-A2.
 PD 22-FEB-2001.
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
 Query Match 5.8%; Score 69.5; DB 4; Length 382;
 Best Local Similarity 20.2%; Pred. No. 67;
 RESULT 1297
 ID ABG7609 standard; protein; 382 AA.
 DE Human lysophosphatidic acid (LPA) receptor EDG-1.
 PN US6485922-B1.
 PD 26-NOV-2002.
 PA (ATAI-) ATAIRGIN TECHNOLOGIES INC.
 Query Match 5.8%; Score 69.5; DB 6; Length 382;
 Best Local Similarity 20.2%; Pred. No. 67;
 RESULT 1298
 ID ABB47613 standard; protein; 400 AA.
 DE Listeria monocytogenes protein #317.
 PN W0200177335-A2.
 PD 18-OCT-2001.
 PA (INSP) INST PASTERUR.
 Query Match 5.8%; Score 69.5; DB 5; Length 400;
 Best Local Similarity 22.9%; Pred. No. 72;
 RESULT 1299
 ID ABU3269 standard; protein; 400 AA.
 DE Protein encoded by Prokaryotic essential gene #18225.
 PN W0200277183-A2.
 PD 03-OCT-2002.
 PA (ELIT-) ELITRA PHARM INC.
 Query Match 5.8%; Score 69.5; DB 6; Length 400;
 Best Local Similarity 22.9%; Pred. No. 72;
 RESULT 1300
 ID ADL12060 standard; protein; 401 AA.
 DE Drosophila dmt1p1 protein.
 PN W02003002137-A2.
 PD 09-JAN-2003.
 PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.

Query Match 5.8%; Score 69.5; DB 7; Length 401;
 Best Local Similarity 20.9%; Pred. No. 72;
 RESULT 1301
 ID ABB60948 standard; protein; 415 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 9636.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 5.8%; Score 69.5; DB 4; Length 415;
 Best Local Similarity 20.9%; Pred. No. 75;
 RESULT 1302
 ID ADL12059 standard; protein; 415 AA.
 DE Drosophila dmt1p12 protein.
 PN W02003002137-A2.
 PD 09-JAN-2003.
 PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
 Query Match 5.8%; Score 69.5; DB 7; Length 415;
 Best Local Similarity 20.9%; Pred. No. 75;
 RESULT 1303
 ID ABB66992 standard; protein; 428 AA.
 DE Drosophila melanogaster polypeptide SEQ ID NO 27768.
 PN W0200171042-A2.
 PD 27-SEP-2001.
 PA (PEKE) PE CORP NY.
 Query Match 5.8%; Score 69.5; DB 4; Length 428;
 Best Local Similarity 20.9%; Pred. No. 79;
 RESULT 1304
 ID ADL12058 standard; protein; 428 AA.
 DE Drosophila dmt1p12 protein.
 PN W02003002137-A2.
 PD 09-JAN-2003.
 PA (DEVE-) DEVELOGEN ENTWICKLUNGSBIOLOGISCHE FORSCH.
 Query Match 5.8%; Score 69.5; DB 7; Length 428;
 Best Local Similarity 20.9%; Pred. No. 79;
 RESULT 1305
 ID AAY41284 standard; protein; 444 AA.
 DE ci-NR-his fusion protein encoded by plasmid pLJM6-09.
 PN W09953033-A1.
 PD 21-OCT-1999.
 PA (UYVA-) UNIV VANDERBILT.
 Query Match 5.8%; Score 69.5; DB 2; Length 444;
 Best Local Similarity 23.6%; Pred. No. 83;
 RESULT 1306
 ID AAG30875 standard; protein; 453 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36988.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 5.8%; Score 69.5; DB 3; Length 453;
 Best Local Similarity 23.3%; Pred. No. 85;
 RESULT 1307
 ID ADK47327 standard; protein; 453 AA.
 DE Streptococcus pneumoniae protein, Seq ID No 3842.
 PN US6699703-B1.
 PD 02-MAR-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.8%; Score 69.5; DB 8; Length 453;
 Best Local Similarity 24.4%; Pred. No. 85;
 RESULT 1308
 ID ADR95087 standard; protein; 461 AA.
 DE Novel S. pneumoniae protein sequence, SEQ ID 3722.
 PN US6800744-B1.
 PD 05-OCT-2004.
 PA (GENO-) GENOME THERAPEUTICS CORP.
 Query Match 5.8%; Score 69.5; DB 8; Length 461;
 Best Local Similarity 24.4%; Pred. No. 87;
 RESULT 1309
 ID AAG30874 standard; protein; 476 AA.
 DE Arabidopsis thaliana protein fragment SEQ ID NO: 36987.
 PN EP1033405-A2.
 PD 06-SEP-2000.
 Query Match 5.8%; Score 69.5; DB 3; Length 476;
 Best Local Similarity 23.3%; Pred. No. 91;
 RESULT 1310

ID ADN22349 standard; protein; 477 AA.
DE Bacterial polypeptide #5002.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 477;
Best Local Similarity 23.5%; Pred. No. 92;
RESULT 1311
ID ADS28512 standard; protein; 490 AA.
DE Bacterial polypeptide #17545.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 490;
Best Local Similarity 21.2%; Pred. No. 95;
RESULT 1312
ID ABO61637 standard; protein; 494 AA.
DE Klebsiella pneumoniae polypeptide seqid 8154.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 494;
Best Local Similarity 22.0%; Pred. No. 96;
RESULT 1313
ID AAY41278 standard; protein; 500 AA.
DE Fusion protein containing rabbit prostaglandin EPZEP3 receptor.
PN WO9933033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 500;
Best Local Similarity 23.6%; Pred. No. 98;
RESULT 1314
ID AAG30873 standard; protein; 503 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 36986.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69.5; DB 3; Length 503;
Best Local Similarity 23.3%; Pred. No. 99;
RESULT 1315
ID AAY92829 standard; protein; 535 AA.
DE C. pneumoniae CPN100557 processed antigen.
PN WO200024765-A2.
PD 04-MAY-2000.
PA (CONN-) CONNUGHT LAB LTD.
Query Match 5.8%; Score 69.5; DB 3; Length 535;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1316
ID ADR13717 standard; protein; 540 AA.
DE Amidase, SEQ ID 54.
PN WO2004069848-A2.
PD 19-AUG-2004.
PA (DIVE-) DIVERSA CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 540;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1317
ID AAY92828 standard; protein; 547 AA.
DE C. pneumoniae CPN100557 antigen.
PN WO200024765-A2.
PD 04-MAY-2000.
PA (CONN-) CONNUGHT LAB LTD.
Query Match 5.8%; Score 69.5; DB 3; Length 547;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1318
ID ABU26764 standard; protein; 547 AA.
DE Protein encoded by prokaryotic essential gene #12291.

PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 547;
Best Local Similarity 21.4%; Pred. No. 1.1e+02;
RESULT 1319
ID ABU31940 standard; protein; 551 AA.
DE Protein encoded by prokaryotic essential gene #17467.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 551;
Best Local Similarity 23.6%; Pred. No. 1.1e+02;
RESULT 1320
ID AAY01650 standard; protein; 557 AA.
DE A protein with cation transporting activity.
PN WO9933072-A1.
PD 18-MAR-1999.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 2; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1321
ID AAY83929 standard; protein; 557 AA.
DE Human carnitine transporter protein OCTN2.
PN WO200014210-A1.
PD 16-MAR-2000.
PA (CHUG-) CHUGAI RES INST MOLECULAR MEDICINE INC.
Query Match 5.8%; Score 69.5; DB 3; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1322
ID ABO3029 standard; protein; 557 AA.
DE Novel human diagnostic protein #3020.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 4; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1323
ID ABB82979 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 3242598.
PN WO200299053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1324
ID ABB82980 standard; protein; 557 AA.
DE Human SLC22A related protein-GenBank Identifier No. GI# 4507005.
PN WO200299053-A2.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1325
ID ABO07242 standard; protein; 557 AA.
DE Human p53 modifying protein, SEQ ID 202.
PN WO200299122-A1.
PD 12-DEC-2002.
PA (EXEL-) EXELIXIS INC.
Query Match 5.8%; Score 69.5; DB 6; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1326
ID ADE09321 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #387.
PN WO2003054152-A2.
PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1327
ID ADE09361 standard; protein; 557 AA.
DE Novel protein-related contig polypeptide sequence #327.
PN WO2003054152-A2.

PD 03-JUL-2003.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69.5; DB 7; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1328
ID ADP23817 standard; protein; 557 AA.
DE PRO polypeptide seq ID NO:995.
PN WO2004041170-A2.
PD 21-MAY-2004.
PA (GETH-) GENENTECH INC.
Query Match 5.8%; Score 69.5; DB 8; Length 557;
Best Local Similarity 26.3%; Pred. No. 1.1e+02;
RESULT 1329
ID ADA34637 standard; protein; 559 AA.
DE Acinetobacter baumannii protein #1798.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 559;
Best Local Similarity 20.2%; Pred. No. 1.1e+02;
RESULT 1330
ID ABO62908 standard; protein; 564 AA.
DE Klebsiella pneumoniae polypeptide seqid 9425.
PN US6610836-B1.
PD 26-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 564;
Best Local Similarity 23.6%; Pred. No. 1.2e+02;
RESULT 1331
ID ABB89665 standard; protein; 568 AA.
DE Human polypeptide seq ID NO 2041.
PN WO200190304-A2.
PD 29-NOV-2001.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.8%; Score 69.5; DB 5; Length 568;
Best Local Similarity 22.4%; Pred. No. 1.2e+02;
RESULT 1332
ID ADB65515 standard; protein; 573 AA.
DE Human protein encoded by clone TEST120271790.
PN EP1308459-A2.
PD 07-MAY-2003.
PA (HELI-) HELIX RES INST.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 69.5; DB 7; Length 573;
Best Local Similarity 22.7%; Pred. No. 1.2e+02;
RESULT 1333
ID ABB47410 standard; protein; 579 AA.
DE Listeria monocytogenes protein #114.
PN WO200177335-A2.
PD 18-OCT-2001.
PA (INSP-) INST PASTERUR.
Query Match 5.8%; Score 69.5; DB 5; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.2e+02;
RESULT 1334
ID ABB32703 standard; protein; 579 AA.
DE Protein encoded by Prokaryotic essential gene #18230.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 579;
Best Local Similarity 21.1%; Pred. No. 1.2e+02;
RESULT 1335
ID ABB65234 standard; protein; 599 AA.
DE Hypoxia-regulated protein #108.
PN WO200246465-A2.
PD 13-JUN-2002.
PA (OXFO-) OXFORD BIOMEDICA UK LTD.
Query Match 5.8%; Score 69.5; DB 5; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.3e+02;
RESULT 1336
ID AAE38584 standard; protein; 599 AA.
DE Human GAT1 GABA transporter protein.
PN WO2003061573-A2.

PD 31-JUL-2003.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.8%; Score 69.5; DB 7; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.3e+02;
RESULT 1337
ID ADD46025 standard; protein; 599 AA.
DE Human Protein P30531, SEQ ID NO 11697.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GEHO-) GEN HOSPITAL CORP.
PA (FARB-) BAYER AG.
Query Match 5.8%; Score 69.5; DB 7; Length 599;
Best Local Similarity 19.6%; Pred. No. 1.3e+02;
RESULT 1338
ID AAY41285 standard; protein; 656 AA.
DE CI-77A-TL fusion protein encoded by plasmid pLJM5-42T.
PN WO9953033-A1.
PD 21-OCT-1999.
PA (UYVA-) UNIV VANDERBILT.
Query Match 5.8%; Score 69.5; DB 2; Length 656;
Best Local Similarity 23.6%; Pred. No. 1.4e+02;
RESULT 1339
ID ABB40194 standard; protein; 660 AA.
DE Staphylococcus epidermidis ORF amino acid sequence SEQ ID NO:5039.
PN US6380370-B1.
PD 30-APR-2002.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 5; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1340
ID ADS07250 standard; protein; 660 AA.
DE Staphylococcus epidermidis polypeptide seqid 6545.
PN US2004147734-A1.
PD 29-JUL-2004.
PA (DOUC-) DODUETTE-STAMM L.
PA (BUSH-) BUSH D.
Query Match 5.8%; Score 69.5; DB 8; Length 660;
Best Local Similarity 27.2%; Pred. No. 1.4e+02;
RESULT 1341
ID AAY17390 standard; protein; 663 AA.
DE Human vesicle membrane protein-like protein 3.
PN WO9921994-A2.
PD 06-MAY-1999.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.8%; Score 69.5; DB 2; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1342
ID ADM83092 standard; protein; 663 AA.
DE Human vesicle membrane protein (VMP)2.
PN US2003175787-A1.
PD 18-SEP-2003.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 69.5; DB 7; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1343
ID ADU64317 standard; protein; 663 AA.
DE Cartilage differentiation inhibiting protein, SEQ ID 12.
PN WO2004013326-A1.
PD 12-FEB-2004.
PA (ASAH-) ASAH KASEI KK.
Query Match 5.8%; Score 69.5; DB 8; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1344
ID ADQ96536 standard; protein; 663 AA.
DE T cell activation associated protein #357.
PN WO2004058805-A2.
PD 15-JUL-2004.
PA (ASAH-) ASAH KASEI PHARMA CORP.
Query Match 5.8%; Score 69.5; DB 8; Length 663;
Best Local Similarity 22.0%; Pred. No. 1.4e+02;
RESULT 1345
ID ADO09827 standard; protein; 681 AA.
DE Hamster SGLT homologue protein SEQ ID NO:50.

PN WO2004039405-A1.
PD 13-MAY-2004.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69.5; DB 8; Length 681;
Best Local Similarity 24.5%; Pred. No. 1.5e+02;
RESULT 1346
ID ABU41908 standard; protein; 695 AA.
DE Protein encoded by Prokaryotic essential gene #27435.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 695;
Best Local Similarity 24.3%; Pred. No. 1.5e+02;
RESULT 1347
ID ADJ48367 standard; protein; 764 AA.
DE Maize oil-associated gene protein #26.
PN US2004025202-A1.
PD 05-FEB-2004.
PA (LAUR/) LAURIE C C.
PA (RAVA/) RAVANELLO M.
PA (SAVA/) SAVAGE T.
PA (LEDE/) LEDEAUX J R.
PA (ROGE/) ROGERS J A.
Query Match 5.8%; Score 69.5; DB 8; Length 764;
Best Local Similarity 21.0%; Pred. No. 1.8e+02;
RESULT 1348
ID ABU43821 standard; protein; 801 AA.
DE Protein encoded by Prokaryotic essential gene #29348.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 801;
Best Local Similarity 19.9%; Pred. No. 1.9e+02;
RESULT 1349
ID AAY70245 standard; protein; 805 AA.
DE Human Polycystin-L protein.
PN WO20012046-A2.
PD 09-MAR-2000.
PA (BGHM) BRIGHAM & WOMENS HOSPITAL INC.
Query Match 5.8%; Score 69.5; DB 3; Length 805;
Best Local Similarity 20.4%; Pred. No. 1.9e+02;
RESULT 1350
ID ABB98140 standard; protein; 863 AA.
DE Human PMW Incyte ID 7484157CD1.
PN WO200246383-A2.
PD 13-JUN-2002.
PA (INCY-) INCYTE GENOMICS INC.
Query Match 5.8%; Score 69.5; DB 5; Length 863;
Best Local Similarity 19.3%; Pred. No. 2.1e+02;
RESULT 1351
ID AAY96168 standard; protein; 877 AA.
DE Saccharomyces cerevisiae OPT protein YPR194C.
PN WO200052162-A2.
PD 08-SEP-2000.
PA (UTTE-) UNIV TENNESSEE RES CORP.
PA (BECK/) BECKER J M.
PA (HAUS/) HAUSER M.
PA (DONH/) DONHARDT A.
PA (BARN/) BARNES D.
Query Match 5.8%; Score 69.5; DB 3; Length 877;
Best Local Similarity 22.7%; Pred. No. 2.1e+02;
RESULT 1352
ID ADS44117 standard; protein; 877 AA.
DE Bacterial polypeptide #22547.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.8%; Score 69.5; DB 8; Length 877;
Best Local Similarity 22.7%; Pred. No. 2.1e+02;

RESULT 1353
ID AAG70761 standard; protein; 881 AA.
DE S cerevisiae apoptosis associated protein YUH197W.
PN WO200102550-A2.
PD 11-JAN-2001.
PA (JANC) JANSSEN PHARM NV.
Query Match 5.8%; Score 69.5; DB 4; Length 881;
Best Local Similarity 24.4%; Pred. No. 2.1e+02;
RESULT 1354
ID ABU16635 standard; protein; 1010 AA.
DE Protein encoded by Prokaryotic essential gene #2162.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69.5; DB 6; Length 1010;
Best Local Similarity 24.7%; Pred. No. 2.6e+02;
RESULT 1355
ID ADA34462 standard; protein; 1028 AA.
DE Acinetobacter Baumannii protein #1623.
PN US6562958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69.5; DB 6; Length 1028;
Best Local Similarity 24.7%; Pred. No. 2.7e+02;
RESULT 1356
ID AAM25671 standard; protein; 1684 AA.
DE hABC3 protein.
PN WO9702346-A2.
PD 23-JAN-1997.
PA (GENZ) GENZYME CORP.
Query Match 5.8%; Score 69.5; DB 2; Length 1684;
Best Local Similarity 20.3%; Pred. No. 5.3e+02;
RESULT 1357
ID AAM46761 standard; protein; 1684 AA.
DE Amino acid sequence of human ATP binding cassette transporter.
PN WO9748797-A1.
PD 24-DEC-1997.
PA (GENZ) GENZYME CORP.
Query Match 5.8%; Score 69.5; DB 2; Length 1684;
Best Local Similarity 20.3%; Pred. No. 5.3e+02;
RESULT 1358
ID AAM46771 standard; protein; 1704 AA.
DE Amino acid sequence of human ATP binding cassette transporter.
PN WO9748797-A1.
PD 24-DEC-1997.
PA (GENZ) GENZYME CORP.
Query Match 5.8%; Score 69.5; DB 2; Length 1704;
Best Local Similarity 20.3%; Pred. No. 5.4e+02;
RESULT 1359
ID ABB52094 standard; protein; 1704 AA.
DE Homo sapiens ABC transporter ABCA3 protein SEQ ID NO:46.
PN EP1217066-A1.
PD 26-JUN-2002.
PA (UYGE-) UNIV GENT.
Query Match 5.8%; Score 69.5; DB 5; Length 1704;
Best Local Similarity 20.3%; Pred. No. 5.4e+02;
RESULT 1360
ID ADJ70414 standard; protein; 1704 AA.
DE Human heat mitochondrial protein as a therapeutic target SeqID2220.
PN WO2003087768-A2.
PD 23-OCT-2003.
PA (MITO-) MITOKOR.
PA (BUCK-) BUCK INST AGE RES.
Query Match 5.8%; Score 69.5; DB 7; Length 1704;
Best Local Similarity 20.3%; Pred. No. 5.4e+02;
RESULT 1361
ID ADU61289 standard; protein; 1704 AA.
DE Human ATP-binding cassette subfamily A (ABCI) member 3 protein.
PN WO2004020583-A2.
PD 11-MAR-2004.
PA (BRIM) BRISTOL-MYERS SQUIBB CO.
Query Match 5.8%; Score 69.5; DB 8; Length 1704;
Best Local Similarity 20.3%; Pred. No. 5.4e+02;

RESULT 1362
ID ABO09274 standard; protein; 154 AA.
DE Ailolococcus otitis antigenic protein SEQ ID NO:3214.
PN W02003048304-A2.
PD 12-JUN-2003.
PA (AMHP) WYETH HOLDINGS CORP.
Query Match 5.8%; Score 69; DB 6; Length 154;
Best Local Similarity 27.3%; Pred. No. 22;
RESULT 1363
ID ADL16543 standard; protein; 178 AA.
DE Nanoarchaeum equitans cancer-associated (CA) protein #247.
PN W02003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match 5.8%; Score 69; DB 8; Length 178;
Best Local Similarity 23.3%; Pred. No. 27;
RESULT 1364
ID AAV65589 standard; protein; 191 AA.
DE Propionibacterium acnes immunogenic protein #26485.
PN W0200181581-A2.
PD 01-NOV-2001.
PA (COR1-) CORIXA CORP.
Query Match 5.8%; Score 69; DB 4; Length 191;
Best Local Similarity 26.6%; Pred. No. 29;
RESULT 1365
ID AAM62108 standard; protein; 191 AA.
DE Propionibacterium acnes permease/transporter-related polypeptide #26784.
PN W02003033515-A1.
PD 24-APR-2003.
PA (COR1-) CORIXA CORP.
Query Match 5.8%; Score 69; DB 6; Length 191;
Best Local Similarity 26.6%; Pred. No. 29;
RESULT 1366
ID AAM38633 standard; protein; 193 AA.
DE S. pneumoniae LPLC protein.
PN W09743303-A1.
PD 20-NOV-1997.
PA (SMIK) SMITHKLINE BEECHAM CORP.
Query Match 5.8%; Score 69; DB 2; Length 193;
Best Local Similarity 28.3%; Pred. No. 30;
RESULT 1367
ID AAB21047 standard; protein; 214 AA.
DE Human nucleic acid-binding protein, NUBP-51.
PN W0200044800-A2.
PD 03-AUG-2000.
PA (INCY-) INCYTE PHARM INC.
Query Match 5.8%; Score 69; DB 3; Length 214;
Best Local Similarity 24.7%; Pred. No. 34;
RESULT 1368
ID ABP58238 standard; protein; 214 AA.
DE Human ovary-specific O1-236 (NPM2) protein.
PN W0200288314-A2.
PD 07-NOV-2002.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 5.8%; Score 69; DB 6; Length 214;
Best Local Similarity 24.7%; Pred. No. 34;
RESULT 1369
ID ADJ63172 standard; protein; 214 AA.
DE Human nucleolepialamin (Npm2) protein.
PN W02003091400-A2.
PD 06-NOV-2003.
PA (BAYU) BAYLOR COLLEGE MEDICINE.
Query Match 5.8%; Score 69; DB 7; Length 214;
Best Local Similarity 24.7%; Pred. No. 34;
RESULT 1370
ID ADM03849 standard; protein; 214 AA.
DE Human protein of the invention SEQ ID NO:2534.
PN EP1347046-A1.
PD 24-SEP-2003.
PA (REAS-) RES ASSOC BIOTECHNOLOGY.
Query Match 5.8%; Score 69; DB 7; Length 214;
Best Local Similarity 24.7%; Pred. No. 34;
RESULT 1371
ID ADN46858 standard; protein; 239 AA.
DE Thermococcus kodakarensis KOD1 protein sequence SegID736.
PN W02004022736-A1.
PD 18-MAR-2004.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.8%; Score 69; DB 8; Length 239;
Best Local Similarity 23.5%; Pred. No. 40;
RESULT 1372
ID AAM63545 standard; protein; 337 AA.
DE Photorhabdus luminescens protein sequence #2642.
PN W0200294867-A2.
PD 28-NOV-2002.
PA (INSP) INST PASTEUR.
Query Match 5.8%; Score 69; DB 6; Length 337;
Best Local Similarity 19.8%; Pred. No. 65;
RESULT 1373
ID AAM72781 standard; protein; 350 AA.
DE Staphylococcus aureus protein #2021.
PN W0200294868-A2.
PD 28-NOV-2002.
PA (CHIR-) CHIRON SPA.
Query Match 5.8%; Score 69; DB 6; Length 350;
Best Local Similarity 20.5%; Pred. No. 68;
RESULT 1374
ID AAG04120 standard; protein; 356 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 27.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 356;
Best Local Similarity 21.0%; Pred. No. 70;
RESULT 1375
ID AAR91218 standard; protein; 370 AA.
DE Human pituitary G-protein coupled receptor protein.
PN W09605102-A1.
PD 22-FEB-1996.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1376
ID AAM31379 standard; protein; 370 AA.
DE Human G-protein-coupled receptor protein from phCR3.
PN W09724436-A2.
PD 10-JUL-1997.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1377
ID AAM95181 standard; peptide; 370 AA.
DE Human G-protein coupled receptor polypeptide.
PN W09849295-A1.
PD 05-NOV-1998.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1378
ID AAM97221 standard; peptide; 370 AA.
DE Human pituitary-derived G-protein-coupled receptor protein.
PN W09858967-A1.
PD 30-DEC-1998.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 2; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1379
ID AAG04119 standard; protein; 370 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 26.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 370;
Best Local Similarity 21.0%; Pred. No. 74;

RESULT 1380
ID AAG62539 standard; protein; 370 AA.
DE Human CRH releasing protein related protein SEQ ID NO: 46.
PN WO200135984-A1.
PD 25-MAY-2001.
PA (TAKE) TAKEEDA CHEM IND LTD.
Query Match 5.8%; Score 69; DB 4; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1381
ID ABB81880 standard; protein; 370 AA.
DE Human G protein-coupled receptor 10 protein SEQ ID NO:245.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match 5.8%; Score 69; DB 6; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1382
ID ADO29365 standard; protein; 370 AA.
DE Human GPCR GPR10, SEQ ID NO:466.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.8%; Score 69; DB 8; Length 370;
Best Local Similarity 21.8%; Pred. No. 74;
RESULT 1383
ID AAM27510 standard; protein; 380 AA.
DE Consensus human hypothalamic receptor.
PN WO9708317-A2.
PD 06-MAR-1997.
PA (CHIR) CHIRON CORP.
Query Match 5.8%; Score 69; DB 2; Length 380;
Best Local Similarity 21.8%; Pred. No. 76;
RESULT 1384
ID AAB16020 standard; protein; 388 AA.
DE E. coli proliferation associated protein sequence SEQ ID NO:378.
PN WO200044506-A2.
PD 03-AUG-2000.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 3; Length 388;
Best Local Similarity 27.2%; Pred. No. 79;
RESULT 1385
ID AAG98322 standard; protein; 388 AA.
DE Escherichia coli protein sequence SEQ ID NO:370.
PN WO200148209-A2.
PD 05-JUL-2001.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 4; Length 388;
Best Local Similarity 27.2%; Pred. No. 79;
RESULT 1386
ID AAB14818 standard; protein; 388 AA.
DE Protein encoded by Prokaryotic essential gene #345.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.8%; Score 69; DB 6; Length 388;
Best Local Similarity 27.2%; Pred. No. 79;
RESULT 1387
ID ADS45229 standard; protein; 437 AA.
DE Bacterial polypeptide #23659.
PN US200233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.
Query Match 5.8%; Score 69; DB 8; Length 437;
Best Local Similarity 22.4%; Pred. No. 93;
RESULT 1388
ID ABO61901 standard; protein; 472 AA.
DE Klebsiella pneumoniae polypeptide seqid 8418.
PN US6610836-B1.
PD 26-AUG-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69; DB 7; Length 472;
Best Local Similarity 21.3%; Pred. No. 1e+02;
RESULT 1389
ID AAG42138 standard; protein; 508 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52514.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 508;
Best Local Similarity 20.2%; Pred. No. 1.1e+02;
RESULT 1390
ID AAG04118 standard; protein; 509 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 25.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 509;
Best Local Similarity 21.0%; Pred. No. 1.1e+02;
RESULT 1391
ID AAG42137 standard; protein; 520 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 52513.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 520;
Best Local Similarity 20.2%; Pred. No. 1.2e+02;
RESULT 1392
ID ABB59760 standard; protein; 593 AA.
DE Drosophila melanogaster polypeptide SEQ ID NO 6072.
PN WO200171042-A2.
PD 27-SEP-2001.
PA (PEKE) PE CORP NY.
Query Match 5.8%; Score 69; DB 4; Length 593;
Best Local Similarity 22.7%; Pred. No. 1.4e+02;
RESULT 1393
ID AAG31959 standard; protein; 609 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38469.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 609;
Best Local Similarity 21.0%; Pred. No. 1.5e+02;
RESULT 1394
ID AAG31958 standard; protein; 624 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38468.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 624;
Best Local Similarity 21.0%; Pred. No. 1.5e+02;
RESULT 1395
ID AAB05101 standard; protein; 641 AA.
DE Drosophila melanogaster dmksnf.
PN WO200149848-A2.
PD 12-JUL-2001.
PA (GENO-) GENOPTERA LLC.
Query Match 5.8%; Score 69; DB 4; Length 641;
Best Local Similarity 22.7%; Pred. No. 1.6e+02;
RESULT 1396
ID AAG31957 standard; protein; 659 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 38467.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.8%; Score 69; DB 3; Length 659;
Best Local Similarity 21.0%; Pred. No. 1.6e+02;
RESULT 1397
ID ABB11769 standard; peptide; 666 AA.
DE Human d37C10.3 ATPase homologue, SEQ ID NO:2139.
PN WO200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 4; Length 666;
Best Local Similarity 23.4%; Pred. No. 1.7e+02;
RESULT 1398
ID AAM79751 standard; protein; 666 AA.
DE Human protein SEQ ID NO 3397.
PN WO200157190-A2.

PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 4; Length 666;
Best Local Similarity 23.4%; Pred. No. 1.7e+02;
RESULT 1399
ID APO5168 standard; protein; 681 AA.
DE Bacterial polypeptide #1281.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.8%; Score 69; DB 7; Length 681;
Best Local Similarity 21.5%; Pred. No. 1.7e+02;
RESULT 1400
ID APO5288 standard; protein; 791 AA.
DE Human putative spliceosome associated protein (SAP) #52.
PN US2003069803-A1.
PD 10-APR-2003.
PA (REED/) REED R.
PA (ZHOU/) ZHOU Z.
Query Match 5.8%; Score 69; DB 6; Length 791;
Best Local Similarity 24.8%; Pred. No. 2.1e+02;
RESULT 1401
ID AAB4279 standard; protein; 792 AA.
DE Human OREX ORF2543 polypeptide sequence SEQ ID NO:5086.
PN WO200058473-A2.
PD 05-OCT-2000.
PA (CURA-) CURAGEN CORP.
Query Match 5.8%; Score 69; DB 3; Length 792;
Best Local Similarity 24.8%; Pred. No. 2.1e+02;
RESULT 1402
ID ABB62960 standard; protein; 875 AA.
DE Human polypeptide SEQ ID NO 397.
PN WO200218424-A2.
PD 07-MAR-2002.
PA (HYSE-) HYSEQ INC.
Query Match 5.8%; Score 69; DB 5; Length 875;
Best Local Similarity 24.8%; Pred. No. 2.4e+02;
RESULT 1403
ID AAM85143 standard; protein; 891 AA.
DE Human diagnostic and therapeutic pprotein SEQ ID NO:5392.
PN WO2004023973-A2.
PD 25-MAR-2004.
PA (INCY-) INCYTE CORP.
Query Match 5.8%; Score 69; DB 8; Length 891;
Best Local Similarity 19.5%; Pred. No. 2.5e+02;
RESULT 1404
ID ABB90877 standard; protein; 1933 AA.
DE Hericidially active polypeptide SEQ ID NO 88.
PN WO20020210-A2.
PD 07-FEB-2002.
PA (FARB) BAYER AG.
Query Match 5.8%; Score 69; DB 5; Length 1933;
Best Local Similarity 17.4%; Pred. No. 7.3e+02;
RESULT 1405
ID AD195303 standard; protein; 2280 AA.
DE OGP-related Hepatitis C virus (HCV) polypeptide.
PN WO2004002415-A2.
PD 08-JAN-2004.
PA (DAND) DANA FARRER CANCER INST INC.
Query Match 5.8%; Score 69; DB 8; Length 2280;
Best Local Similarity 26.9%; Pred. No. 9.2e+02;
RESULT 1406
ID ADM68764 standard; protein; 5127 AA.
DE Pteroglynnus maidis ryanodine receptor protein SEQ ID NO:8.
PN WO2004027042-A2.
PD 01-APR-2004.
PA (DUPO) DU PONT DE NEMOURS & CO E I.
Query Match 5.8%; Score 69; DB 8; Length 5127;
Best Local Similarity 20.1%; Pred. No. 2.8e+03;
RESULT 1407
ID ADH85829 standard; protein; 178 AA.
DE Enterococcus faecalis polypeptide #309.
PN US6617156-B1.

PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match 5.7%; Score 68.5; DB 7; Length 178;
Best Local Similarity 30.7%; Pred. No. 31;
RESULT 1408
ID ABO1003 standard; protein; 209 AA.
DE Human breast specific protein SEQ ID NO: 86.
PN WO200240672-A2.
PD 23-MAY-2002.
PA (DIAD-) DIADEXUS INC.
Query Match 5.7%; Score 68.5; DB 5; Length 209;
Best Local Similarity 21.8%; Pred. No. 38;
RESULT 1409
ID AAG53772 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68492.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 41;
RESULT 1410
ID AAG25640 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 29784.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 41;
RESULT 1411
ID AAG53747 standard; protein; 218 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 68458.
PN EP1033405-A2.
PD 06-SEP-2000.
Query Match 5.7%; Score 68.5; DB 3; Length 218;
Best Local Similarity 40.7%; Pred. No. 41;
RESULT 1412
ID ADF07413 standard; protein; 225 AA.
DE Bacterial polypeptide #3526.
PN US6605709-B1.
PD 12-AUG-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 225;
Best Local Similarity 18.2%; Pred. No. 42;
RESULT 1413
ID ADO57686 standard; protein; 227 AA.
DE Actinobacillus actinomycetemcomitans immunogenic polypeptide #68.
PN WO2004045499-A2.
PD 03-JUN-2004.
PA (UYFL) UNIV FLORIDA.
Query Match 5.7%; Score 68.5; DB 8; Length 227;
Best Local Similarity 24.3%; Pred. No. 43;
RESULT 1414
ID ADA14398 standard; protein; 278 AA.
DE Mouse spermatogenesis related protein sequence SEQ ID NO:140.
PN WO2003068969-A1.
PD 21-AUG-2003.
PA (NISC-) JAPAN SCI & TECHNOLOGY CORP.
Query Match 5.7%; Score 68.5; DB 6; Length 278;
Best Local Similarity 29.2%; Pred. No. 57;
RESULT 1415
ID ABU29281 standard; protein; 322 AA.
DE Protein encoded by Prokaryotic essential gene #14808.
PN WO200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 6; Length 322;
Best Local Similarity 30.7%; Pred. No. 70;
RESULT 1416
ID ABB99751 standard; protein; 327 AA.
DE Amino acid sequence of bacteriophage phiCpn1 antigenic protein.
PN WO200295413-A2.
PD 28-NOV-2002.
PA (UYBR-) UNIV BRITISH COLUMBIA.
Query Match 5.7%; Score 68.5; DB 6; Length 327;

Best Local Similarity 27.0%; Pred. No. 71;
RESULT 1417
ID AAM25926 standard; protein; 354 AA.
DE Xenopus-melatonin receptor MEL-1A.
PN WO9704094-A1.
PD 06-FEB-1997.
PA (ADIR) ADIR & CIE.
Query Match
Best Local Similarity 18.8%; Pred. No. 79;
RESULT 1418
ID AAY87506 standard; protein; 369 AA.
DE Human G coupled-protein receptor, GPR10.
PN WO20017641-A1.
PD 30-MAR-2000.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match
Best Local Similarity 23.3%; Pred. No. 84;
RESULT 1419
ID AAE13430 standard; protein; 377 AA.
DE Brassica napus microsomal omega-3 desaturase, bnfAD3 protein.
PN WO200179499-A1.
PD 25-OCT-2001.
PA (CSIR) COMMONWEALTH SCI & IND RES ORG.
Query Match
Best Local Similarity 29.3%; Pred. No. 87;
RESULT 1420
ID AAB28521 standard; protein; 382 AA.
DE Mouse EDG1 polypeptide.
PN WO200059529-A1.
PD 12-OCT-2000.
PA (SMIRK) SMITHKLINE BEECHAM CORP.
Query Match
Best Local Similarity 19.8%; Pred. No. 88;
RESULT 1421
ID AAM85456 standard; protein; 382 AA.
DE Mouse protein sequence mcp20760.
PN WO2003073826-A2.
PD 12-SEP-2003.
PA (SAGR-) SAGRES DISCOVERY.
Query Match
Best Local Similarity 19.8%; Pred. No. 88;
RESULT 1422
ID ADO29286 standard; protein; 382 AA.
DE Mouse GPCR EDG1, SEQ ID NO:387.
PN WO200404000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match
Best Local Similarity 19.8%; Pred. No. 88;
RESULT 1423
ID ADR67019 standard; protein; 382 AA.
DE Mouse cancer associated protein sequence SEQ ID NO:65.
PN WO2004074321-A2.
PD 02-SEP-2004.
PA (SAGR-) SAGRES DISCOVERY INC.
Query Match
Best Local Similarity 19.8%; Pred. No. 88;
RESULT 1424
ID AAM01664 standard; protein; 383 AA.
DE P1rat-edg1, G-protein coupled receptor.
PN US5585476-A.
PD 17-DEC-1996.
PA (MACL/) MACLENNAN A J.
Query Match
Best Local Similarity 19.8%; Pred. No. 89;
RESULT 1425
ID AAM87791 standard; protein; 383 AA.
DE Rat-edg, G-protein coupled receptor superfamily member.
PN US5585443-A.
PD 05-JAN-1999.
PA (MACL/) MACLENNAN A J.
Query Match
Best Local Similarity 19.8%; Pred. No. 89;
Length 383;

RESULT 1426
ID ABU61817 standard; protein; 383 AA.
DE Rat-edg.
PN US6518414-B1.
PD 11-FEB-2003.
PA (MACL/) MACLENNAN A J.
Query Match
Best Local Similarity 19.8%; Pred. No. 89;
RESULT 1427
ID ABG07020 standard; protein; 404 AA.
DE Novel human diagnostic protein #7011.
PN WO200175067-A2.
PD 11-OCT-2001.
PA (HYSE-) HYSEQ INC.
Query Match
Best Local Similarity 22.4%; Pred. No. 95;
RESULT 1428
ID AAB68619 standard; protein; 411 AA.
DE Human PAC_1 receptor isoform 30.
PN WO200107478-A1.
PD 01-FEB-2001.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match
Best Local Similarity 29.9%; Pred. No. 98;
RESULT 1429
ID ADH87117 standard; protein; 417 AA.
DE Enterococcus faecalis polypeptide #1597.
PN US6617156-B1.
PD 09-SEP-2003.
PA (DOUC/) DOUCETTE-STAMM L A.
PA (BUSH/) BUSH D.
Query Match
Best Local Similarity 23.2%; Pred. No. 1e+02;
RESULT 1430
ID AAB86409 standard; protein; 420 AA.
DE High-affinity melatonin receptor.
PN WO9535320-A1.
PD 28-DEC-1995.
PA (MASS-) MASSACHUSETTS GEN HOSPITAL.
Query Match
Best Local Similarity 18.8%; Pred. No. 1e+02;
RESULT 1431
ID AAM8344 standard; protein; 430 AA.
DE Salmonella enterica O antigen pathway flippase protein.
PN WO9850531-A1.
PD 12-NOV-1998.
PA (UNSY) UNIV SYDNEY.
Query Match
Best Local Similarity 23.6%; Pred. No. 1e+02;
RESULT 1432
ID AAU02941 standard; protein; 431 AA.
DE Angiotensin converting enzyme (ACEV) splice variant protein #41.
PN WO200136632-A2.
PD 25-MAY-2001.
PA (COMP-) COMPUGEN LTD.
Query Match
Best Local Similarity 29.9%; Pred. No. 1e+02;
RESULT 1433
ID ADA33815 standard; protein; 437 AA.
DE Actinobacter baumannii protein #976.
PN US6362958-B1.
PD 13-MAY-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match
Best Local Similarity 20.5%; Pred. No. 1.1e+02;
RESULT 1434
ID ADS12084 standard; protein; 443 AA.
DE Human therapeutic conlig protein - SEQ ID 2321.
PN WO2004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match
Best Local Similarity 19.6%; Pred. No. 1.1e+02;
Length 443;

RESULT 1435
ID AAB71866 standard; protein; 444 AA.
DE Human CRP seven transmembrane domain.
PN WO200109328-A1.
PD 08-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1436
ID AAE26685 standard; protein; 444 AA.
DE Human CRP-RA2 splice variant protein.
PN US202055617-A1.
PD 09-MAY-2002.
PA (PERR/) PERRIN M H.
PA (CHEN/) CHEN R.
PA (LEW/) LEWIS K A.
PA (VALE/) VALE W W.
PA (DONA/) DONALDSON C J.
PA (SAMC/) SAMCHENKO P.
Query Match 5.7%; Score 68.5; DB 5; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1437
ID ABR43052 standard; protein; 444 AA.
DE Human CRP-RI beta protein SEQ ID NO:2.
PN WO2003024990-A2.
PD 27-MAR-2003.
PA (UYTE-) UNIV TENNESSEE RES CORP.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1438
ID ABU08081 standard; protein; 444 AA.
DE Human corticotropin-releasing factor receptor 2 (CRF-R2).
PN US6496343-B1.
PD 17-DEC-2002.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1439
ID ABG76402 standard; protein; 444 AA.
DE Human hCRP-RA1, splice variant.
PN US6482608-B1.
PD 19-NOV-2002.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 6; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1440
ID ADE62734 standard; protein; 444 AA.
DE Human Protein P34998, SEQ ID NO 8667.
PN WO2003016475-A2.
PD 27-FEB-2003.
PA (GCHO) GEN HOSPITAL CORP.
PA (FARB) BAYER AG.
Query Match 5.7%; Score 68.5; DB 7; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1441
ID ADU65810 standard; protein; 444 AA.
DE Human corticotropin-releasing factor receptor CRF-RA2.
PN US2004035173-A1.
PD 26-FEB-2004.
PA (SALK) SALK INST BIOLOGICAL STUDIES.
Query Match 5.7%; Score 68.5; DB 8; Length 444;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1442
ID ADC86255 standard; protein; 447 AA.
DE Human GPCR protein SEQ ID NO:708.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.7%; Score 68.5; DB 7; Length 447;
Best Local Similarity 23.7%; Pred. No. 1.1e+02;
RESULT 1443
ID AAR58668 standard; protein; 448 AA.

DE Human PACAP receptor type 1A mature protein.
PN EPI18291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 448;
Best Local Similarity 29.9%; Pred. No. 1.1e+02;
RESULT 1444
ID ABB56380 standard; protein; 468 AA.
DE Non-endogenous human GPCR protein, SEQ ID NO: 553.
PN WO200177172-A2.
PD 18-OCT-2001.
PA (AREN-) ARENA PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1445
ID AAB71874 standard; protein; 468 AA.
DE Human PACR seven transmembrane domain.
PN WO200109328-A1.
PD 08-FEB-2001.
PA (MILL-) MILLENNIUM PHARM INC.
Query Match 5.7%; Score 68.5; DB 4; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1446
ID ADC86185 standard; protein; 468 AA.
DE Human GPCR protein SEQ ID NO:638.
PN EPI270724-A2.
PD 02-JAN-2003.
PA (NAD-) NAT INST ADVANCED IND SCI & TECHNOLOGY.
PA (ADSC-) CENT ADVANCED SCI & TECHNOLOGY INCUBATIO.
Query Match 5.7%; Score 68.5; DB 7; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1447
ID ADO29153 standard; protein; 468 AA.
DE Human GPCR ADCYAP1R1, SEQ ID NO:254.
PN WO2004040000-A2.
PD 13-MAY-2004.
PA (PRIM-) PRIMAL INC.
Query Match 5.7%; Score 68.5; DB 8; Length 468;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1448
ID AAR58670 standard; protein; 475 AA.
DE Human PACAP receptor type 1-B2 mature protein.
PN EPI18291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 475;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1449
ID AAR58671 standard; protein; 476 AA.
DE Human PACAP receptor type 1C mature protein.
PN EPI18291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 476;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1450
ID AAR58669 standard; protein; 476 AA.
DE Human PACAP receptor type 1B mature protein.
PN EPI18291-A2.
PD 05-OCT-1994.
PA (TAKE) TAKEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 476;
Best Local Similarity 29.9%; Pred. No. 1.2e+02;
RESULT 1451
ID ADN24160 standard; protein; 488 AA.
DE Bacterial polypeptide #6813.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY) CAO Y.
PA (HINK) HINKLE G J.
PA (SLAT) SLATER S C.
PA (CHEN) CHEN X.
PA (GOLD) GOLDMAN B S.

Query Match
Best Local Similarity 5.7%; Score 68.5; DB 8; Length 488;
RESULT 1452
ID ABB65829 standard; protein; 495 AA.
DE Bifidobacterium longum NCC2705 ORF amino acid sequence SEQ ID NO:573.
PN EPI227152-A1.
PD 31-JUL-2002.
PA (NEST) SOC PROD NESTLE SA.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 5; Length 495;
RESULT 1453
ID ABB68618 standard; protein; 524 AA.
DE Human PAC 1 receptor.
PN WO200107478-A1.
PD 01-FEB-2001.
PA (MEDI-) MEDICAL RES COUNCIL.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 4; Length 524;
RESULT 1454
ID AAR58659 standard; protein; 525 AA.
DE Human PACAP receptor type 1A protein.
PN EPI18291-A2.
PD 05-OCT-1994.
PA (TAKA) TAKEDA CHEM IND LTD.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 2; Length 525;
RESULT 1455
ID ABH08611 standard; protein; 525 AA.
DE Human pituitary adenylate cyclase (PAC) 1 receptor.
PN US2002182729-A1.
PD 05-DEC-2002.
PA (DICI/) DICICCO-BLOOM E.
PA (NICO/) NICOT A.
PA (LUNN/) LU N.
PA (SUHJ/) SUH J.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 6; Length 525;
RESULT 1456
ID ABB81873 standard; protein; 525 AA.
DE Human PACAP receptor type 1 protein SEQ ID NO:231.
PN WO200261087-A2.
PD 08-AUG-2002.
PA (LIFE-) LIFESPAN BIOSCIENCES INC.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 6; Length 525;
RESULT 1457
ID ADN38958 standard; protein; 525 AA.
DE Cancer/angiogenesis/fibrosis-related polypeptide, SEQ ID NO:276.
PN WO2003042661-A2.
PD 22-MAY-2003.
PA (EOSB-) EOS BIOTECHNOLOGY INC.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 7; Length 525;
RESULT 1458
ID ABB73995 standard; protein; 541 AA.
DE Candida albicans essential protein SEQ ID NO 7832.
PN WO200253728-A2.
PD 11-JUL-2002.
PA (BLIT-) BLITTA PHARM INC.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 5; Length 541;
RESULT 1459
ID ABG95329 standard; protein; 548 AA.
DE Human novel secreted protein #150.
PN US6420526-B1.
PD 16-JUL-2002.
PA (HUMA-) HUMAN GENOME SCI INC.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 5; Length 548;
RESULT 1460
ID ABO34523 standard; protein; 548 AA.
DE Region of human secreted protein encoded by cDNA sequence #150.
PN US2003049618-A1.

PD 13-MAR-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJU/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJU/) HU J.
PA (FLOA/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 7; Length 548;
RESULT 1461
ID ADI23184 standard; protein; 548 AA.
DE Novel human secreted protein seq id 469.
PN US2003175858-A1.
PD 18-SEP-2003.
PA (RUBE/) RUBEN S M.
PA (ROSE/) ROSEN C A.
PA (SOPP/) SOPPET D R.
PA (CART/) CARTER K C.
PA (BEDN/) BEDNARIK D P.
PA (ENDR/) ENDRESS G A.
PA (YUGG/) YU G.
PA (NIJU/) NI J.
PA (FENG/) FENG P.
PA (YOUN/) YOUNG P E.
PA (GREE/) GREENE J M.
PA (FERR/) FERRIE A M.
PA (DUAN/) DUAN D R.
PA (HUJU/) HU J.
PA (FLOA/) FLORENCE K A.
PA (OLSE/) OLSEN H S.
PA (FISC/) FISCHER C L.
PA (EBNE/) EBNER R.
PA (BREW/) BREWER L A.
PA (MOOR/) MOORE P A.
PA (SHIY/) SHI Y.
PA (LAFL/) LAFLEUR D W.
PA (LIYY/) LI Y.
PA (ZENG/) ZENG Z.
PA (KYAW/) KYAW H.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 8; Length 548;
RESULT 1462
ID ADH17089 standard; protein; 548 AA.
DE Human translation initiation factor eIF3 p66 subunit protein.
PN WO2003097854-A2.
PD 27-NOV-2003.
PA (SUGB-) SUGEN INC.
Query Match
Best Local Similarity 5.7%; Score 68.5; DB 8; Length 548;
RESULT 1463
ID ADH74186 standard; protein; 548 AA.
DE Human secreted protein #150.
PN US2003225248-A1.
PD 04-DEC-2003.

PA (HUMA-) HUMAN GENOME SCI INC.
Query Match 5.7%; Score 68.5; DB 8; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1464
ID ASM82346 standard; protein: 548 AA.
DE Tumour-associated antigenic target (TAT) polypeptide PRO22481, SEQ:6028.
PN W02004030615-A2.
PD 15-APR-2004.
PA (GETH-) GENENTECH INC.
Query Match 5.7%; Score 68.5; DB 8; Length 548;
Best Local Similarity 34.0%; Pred. No. 1.5e+02;
RESULT 1465
ID AAR58661 standard; protein: 552 AA.
DE Human PACAP receptor type 1-B2 protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE-) TAKEEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 552;
Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1466
ID AAR58662 standard; protein: 553 AA.
DE Human PACAP receptor type 1C protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE-) TAKEEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 553;
Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1467
ID AAR58660 standard; protein: 553 AA.
DE Human PACAP receptor type 1B protein.
PN EP618291-A2.
PD 05-OCT-1994.
PA (TAKE-) TAKEEDA CHEM IND LTD.
Query Match 5.7%; Score 68.5; DB 2; Length 553;
Best Local Similarity 29.9%; Pred. No. 1.5e+02;
RESULT 1468
ID ABB11705 standard; peptide: 588 AA.
DE Human GABA transporter homologue, SEQ ID NO:2075.
PN W0200157188-A2.
PD 09-AUG-2001.
PA (HYSE-) HYSEQ INC.
Query Match 5.7%; Score 68.5; DB 4; Length 588;
Best Local Similarity 19.6%; Pred. No. 1.6e+02;
RESULT 1469
ID ADP98892 standard; protein: 597 AA.
DE C. albicans specific gene, orf6.4254, protein sequence.
PN W02004056965-A2.
PD 08-JUL-2004.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 8; Length 597;
Best Local Similarity 26.2%; Pred. No. 1.6e+02;
RESULT 1470
ID ADS10834 standard; protein: 600 AA.
DE Human therapeutic protein - SEQ ID 1071.
PN W02004080148-A2.
PD 23-SEP-2004.
PA (NUVE-) NUVELO INC.
Query Match 5.7%; Score 68.5; DB 8; Length 600;
Best Local Similarity 19.6%; Pred. No. 1.6e+02;
RESULT 1471
ID ABB38306 standard; protein: 634 AA.
DE Protein encoded by Prokaryotic essential gene #28333.
PN W0200277183-A2.
PD 03-OCT-2002.
PA (ELIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 6; Length 634;
Best Local Similarity 26.3%; Pred. No. 1.8e+02;
RESULT 1472
ID ABO81139 standard; protein: 660 AA.
DE Pseudomonas aeruginosa polypeptide #13314.
PN US6551795-B1.
PD 22-APR-2003.

PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 660;
Best Local Similarity 26.3%; Pred. No. 1.9e+02;
RESULT 1473
ID AAG20246 standard; protein: 663 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22359.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 3; Length 663;
Best Local Similarity 22.3%; Pred. No. 1.9e+02;
RESULT 1474
ID ABB53933 standard; protein: 670 AA.
DE Lactococcus lactis protein kxp1.
PN PR2807446-A1.
PD 12-OCT-2001.
PA (INRG-) INRA INST NAT RECH AGRONOMIQUE.
Query Match 5.7%; Score 68.5; DB 5; Length 670;
Best Local Similarity 22.1%; Pred. No. 1.9e+02;
RESULT 1475
ID ABB50927 standard; protein: 691 AA.
DE Helicobacter pylori selected interacting domain (SID) protein #270.
PN W0200266501-A2.
PD 29-AUG-2002.
PA (HYBR-) HYBRIGENICS.
PA (INSP-) INST PASTEUR.
Query Match 5.7%; Score 68.5; DB 5; Length 691;
Best Local Similarity 19.2%; Pred. No. 2e+02;
RESULT 1476
ID AAG20245 standard; protein: 704 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22358.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 3; Length 704;
Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1477
ID AAG20244 standard; protein: 724 AA.
DE Arabidopsis thaliana protein fragment SEQ ID NO: 22357.
PN EP1033405-A2.
PD 06-SEP-2000.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 3; Length 724;
Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1478
ID AAU72535 standard; protein: 724 AA.
DE Arabidopsis cell cycle protein CCP25.
PN W0200185946-A2.
PD 15-NOV-2001.
PA (CROP-) CROPDISEIGN NV.
Query Match 5.7%; Score 68.5; DB 5; Length 724;
Best Local Similarity 22.3%; Pred. No. 2.1e+02;
RESULT 1479
ID ADS23914 standard; protein: 731 AA.
DE Bacterial polypeptide #12947.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 68.5; DB 8; Length 731;
Best Local Similarity 25.9%; Pred. No. 2.2e+02;
RESULT 1480
ID ADC95469 standard; protein: 738 AA.
DE E. faecium protein sequence SEQ ID 5096.
PN US6583275-B1.
PD 24-JUN-2003.
PA (GENO-) GENOME THERAPEUTICS CORP.
Query Match 5.7%; Score 68.5; DB 7; Length 738;
Best Local Similarity 20.3%; Pred. No. 2.2e+02;
RESULT 1481
ID AAB46310 standard; protein: 788 AA.
DE H. pylori Hsp115 protein.
PN W0200073502-A2.

PD 07-DEC-2000.
PA (PLAC-) MAX PLANCK GES FORBORDERUNG WISSENSCHAFTEN.
PA (CREA-) CREATOGEN GMBH.
Query Match 5.7%; Score 68.5; DB 4; Length 788;
Best Local Similarity 19.2%; Pred. No. 2.4e+02;
RESULT 1482
ID AAY92103 standard; protein; 885 AA.
DE Human WFS1 mutant DEL508 YYLL.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 885;
Best Local Similarity 23.8%; Pred. No. 2.8e+02;
RESULT 1483
ID AAY92105 standard; protein; 890 AA.
DE Human WFS1 mutant G695V.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1484
ID AAY92107 standard; protein; 890 AA.
DE Human WFS1 mutant F504L.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1485
ID AAY92110 standard; protein; 890 AA.
DE Human WFS1 polymorphism I333V.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1486
ID AAY92109 standard; protein; 890 AA.
DE Human WFS1 polymorphism R456H.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1487
ID AAY92100 standard; protein; 890 AA.
DE WFS1 polypeptide.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1488
ID AAY92104 standard; protein; 890 AA.

DE Human WFS1 mutant P724L.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 890;
Best Local Similarity 23.8%; Pred. No. 2.9e+02;
RESULT 1489
ID ABP29861 standard; protein; 894 AA.
DE Streptococcus polypeptide SEQ ID NO 8898.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.7%; Score 68.5; DB 5; Length 894;
Best Local Similarity 22.9%; Pred. No. 2.9e+02;
RESULT 1490
ID ABP28153 standard; protein; 894 AA.
DE Streptococcus polypeptide SEQ ID NO 5482.
PN WO200234771-A2.
PD 02-MAY-2002.
PA (CHIR-) CHIRON SPA.
PA (GENO-) INST GENOMIC RES.
Query Match 5.7%; Score 68.5; DB 5; Length 894;
Best Local Similarity 22.9%; Pred. No. 2.9e+02;
RESULT 1491
ID AAY92102 standard; protein; 937 AA.
DE Human WFS1 mutant del828fs/ter937.
PN WO200018787-A1.
PD 06-APR-2000.
PA (UNIW) UNIV WASHINGTON.
PA (PERM/) PERMUTT M A.
PA (INOU/) INOUE H.
PA (MUEC/) MUECKLER M.
Query Match 5.7%; Score 68.5; DB 3; Length 937;
Best Local Similarity 23.8%; Pred. No. 3.1e+02;
RESULT 1492
ID ADN19015 standard; protein; 1004 AA.
DE Bacterial polypeptide #1668.
PN US2003233675-A1.
PD 18-DEC-2003.
PA (CAOY/) CAO Y.
PA (HINK/) HINKLE G J.
PA (SLAT/) SLATER S C.
PA (CHEN/) CHEN X.
PA (GOLD/) GOLDMAN B S.
Query Match 5.7%; Score 68.5; DB 8; Length 1004;
Best Local Similarity 19.6%; Pred. No. 3.4e+02;
RESULT 1493
ID ADB70303 standard; protein; 1178 AA.
DE C. neoformans amino acid sequence SEQ ID NO:3347.
PN WO2003052076-A2.
PD 26-JUN-2003.
PA (BLIT-) ELITRA PHARM INC.
Query Match 5.7%; Score 68.5; DB 7; Length 1178;
Best Local Similarity 19.8%; Pred. No. 4.2e+02;
RESULT 1494
ID AAM88448 standard; protein; 1296 AA.
DE Caenorhabditis elegans NPCL protein orthologue.
PN WO9901555-A1.
PD 14-JAN-1999.
PA (USSH) US DEPT HEALTH & HUMAN RESOURCES.
Query Match 5.7%; Score 68.5; DB 2; Length 1296;
Best Local Similarity 25.8%; Pred. No. 4.8e+02;
RESULT 1495
ID AAB30730 standard; protein; 3015 AA.
DE Amino acid sequence of chimeric Hepatitis C virus clone pH77CV-J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (USSH) US DEPT HEALTH & HUMAN SERVICES.
Query Match 5.7%; Score 68.5; DB 4; Length 3015;

Best Local Similarity 26.7%; Pred. No. 1.5e+03;
RESULT 1496
ID AAB30732 standard; protein; 3015 AA.
DE Amino acid sequence of chimeric Hepatitis C virus clone J6S.
PN WO200075338-A2.
PD 14-DEC-2000.
PA (US9H) US DEPT HEALTH & HUMAN SERVICES.
Query Match
Best Local Similarity 26.7%; Pred. No. 1.5e+03; Length 3015;
RESULT 1497
ID ADK16845 standard; protein; 200 AA.
DE Nanorarchaeum equitans cancer-associated (CA) protein #398.
PN WO2003093434-A2.
PD 13-NOV-2003.
PA (DIVE-) DIVERSA CORP.
Query Match
Best Local Similarity 23.5%; Pred. No. 41; Length 200;
RESULT 1498
ID AAB78946 standard; protein; 247 AA.
DE C. glutamicum SRT protein sequence SEQ ID NO:152.
PN WO200100804-A2.
PD 04-JAN-2001.
PA (BADI) BASF AG.
Query Match
Best Local Similarity 23.1%; Pred. No. 55; Length 247;
RESULT 1499
ID AAG91355 standard; protein; 247 AA.
DE C glutamicum protein fragment SEQ ID NO: 5109.
PN EP108790-A2.
PD 20-JUN-2001.
PA (KYOW) KYOWA HAKKO KOGYO KK.
Query Match
Best Local Similarity 23.1%; Pred. No. 55; Length 247;
RESULT 1500
ID AAY41212 standard; protein; 258 AA.
DE E. coli MCB polypeptide.
PN WO9951753-A1.
PD 14-OCT-1999.
PA (UTAL-) UNITV ALBERTA.
Query Match
Best Local Similarity 23.0%; Pred. No. 59; Length 258;

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OM protein - protein search, using BW model

Run on: May 17, 2005, 10:22:46 ; Search time 138 Seconds
(without alignments)
566.436 Million cell updates/sec

Perfect score: 1195
Sequence: 1 NMHLPRDMENALTGSSQSHA.....EAGSEAEKQDEKFLLEL 234

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1432185 seqs, 334051727 residues

Total number of hits satisfying chosen parameters: 1432185

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 1500 summaries

Database :

Published Applications AA:*

- 1: /cgn2_6/prodata/2/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/prodata/2/pubppaa/PCF_NEW_PUB.pep:*
- 3: /cgn2_6/prodata/2/pubppaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/prodata/2/pubppaa/US06_PUBCOMB.pep:*
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- 9: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/prodata/2/pubppaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/prodata/2/pubppaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/prodata/2/pubppaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/prodata/2/pubppaa/US10_PUBCOMB.pep:*
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- 18: /cgn2_6/prodata/2/pubppaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/prodata/2/pubppaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/prodata/2/pubppaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
449	1195	100.0	234	14	US-10-223-085-62
446	1195	100.0	234	14	US-10-223-084-62
467	1195	100.0	234	14	US-10-223-088-62
468	1195	100.0	234	14	US-10-223-090-62
470	1195	100.0	234	14	US-10-223-087-62
478	1195	100.0	234	14	US-10-223-083-62
481	1195	100.0	234	14	US-10-223-089-62
498	1195	100.0	234	14	US-10-174-587-66
562	1195	100.0	234	14	US-10-063-742-14
640	1195	100.0	234	14	US-10-223-081-62
650	1195	100.0	234	14	US-10-223-082-62
665	1195	100.0	234	14	US-10-144-194A-20
670	1195	100.0	234	15	US-10-305-654-62
675	1195	100.0	234	15	US-10-081-056-62

681	1195	100.0	234	17	US-10-972-317-14	Sequence 14, Appl
682	1188	99.4	234	15	US-10-262-839-84	Sequence 84, Appl
683	1024	85.7	201	15	US-10-264-237-2663	Sequence 2663, Ap
684	985	82.4	198	15	US-10-262-839-82	Sequence 82, Appl
685	669.5	56.0	176	15	US-10-104-047-2567	Sequence 2567, Ap
686	664	55.6	445	15	US-10-177-293-296	Sequence 296, App
687	664	55.6	445	15	US-10-435-696-33	Sequence 33, Appl
688	578	48.4	412	17	US-10-491-213-22	Sequence 22, Appl
689	91	7.6	373	14	US-10-091-007-198	Sequence 198, App
690	90.5	7.6	803	16	US-10-437-963-136814	Sequence 136814,
691	87.5	7.3	516	9	US-09-925-898-653	Sequence 653, App
692	87.5	7.3	516	14	US-10-102-806-653	Sequence 653, App
693	87	7.3	421	17	US-10-741-600-929	Sequence 929, App
694	85.5	7.2	223	17	US-10-741-600-926	Sequence 926, App
695	85.5	7.2	285	17	US-10-741-600-921	Sequence 921, App
696	85.5	7.2	315	17	US-10-741-600-925	Sequence 925, App
697	85.5	7.2	323	17	US-10-741-600-923	Sequence 923, App
698	85.5	7.2	328	17	US-10-741-600-924	Sequence 924, App
699	85.5	7.2	338	17	US-10-741-600-928	Sequence 928, App
700	85.5	7.2	339	17	US-10-741-600-930	Sequence 930, App
701	85.5	7.2	384	17	US-10-741-600-932	Sequence 932, App
702	85.5	7.2	390	17	US-10-741-600-927	Sequence 927, App
703	85.5	7.2	336	15	US-10-282-122A-34604	Sequence 54604, A
704	85.5	7.2	438	17	US-10-741-600-931	Sequence 931, App
705	85.5	7.2	440	15	US-10-262-511-182	Sequence 182, App
706	85.5	7.2	473	15	US-10-264-237-2016	Sequence 2016, Ap
707	85.5	7.2	500	15	US-10-282-122A-68468	Sequence 68468, A
708	85	7.1	527	15	US-10-425-114-65247	Sequence 65247, A
709	85	7.1	797	14	US-10-156-761-11433	Sequence 11433, A
710	84.5	7.1	430	15	US-10-282-122A-61134	Sequence 61134, A
711	84.5	6.9	886	16	US-10-437-963-111543	Sequence 111543,
712	82.5	6.9	239	15	US-10-282-122A-63532	Sequence 63532, A
713	82.5	6.9	341	14	US-10-216-209-92	Sequence 92, Appl
714	82	6.9	289	14	US-10-205-194-144	Sequence 144, App
715	81.5	6.8	349	15	US-10-425-114-44166	Sequence 44166, A
716	81.5	6.8	436	15	US-10-424-599-272132	Sequence 272132,
717	81.5	6.8	659	16	US-10-437-963-128426	Sequence 128426,
718	81	6.8	529	15	US-10-369-493-5808	Sequence 5808, Ap
719	81	6.8	529	15	US-10-369-493-5809	Sequence 5809, Ap
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721	80.5	6.7	891	14	US-10-226-628A-16	Sequence 16, Appl
722	80	6.7	144	9	US-09-925-297-851	Sequence 851, Appl
723	80	6.7	238	15	US-10-108-260A-3158	Sequence 3158, Ap
724	80	6.7	360	11	US-09-833-245-1308	Sequence 1308, Ap
725	80	6.7	536	15	US-10-425-114-37103	Sequence 37103, A
726	80	6.7	531	15	US-10-424-599-169136	Sequence 169136,
727	79.5	6.7	355	15	US-10-282-122A-53478	Sequence 53478, A
728	79.5	6.7	406	14	US-10-223-538-4	Sequence 4, Appl1
729	79.5	6.7	723	15	US-10-257-023-4	Sequence 4, Appl1
730	79	6.6	121	15	US-10-335-977-8880	Sequence 8880, Ap
731	79	6.6	1531	15	US-10-353-699-110	Sequence 110, App
732	79	6.6	1537	9	US-09-832-892-35	Sequence 35, Appl
733	78.5	6.6	135	14	US-10-029-386-29323	Sequence 29323, A
734	78.5	6.6	239	15	US-10-282-122A-64222	Sequence 64222, A
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736	78.5	6.6	766	13	US-10-072-621-6	Sequence 6, Appl1
737	78.5	6.6	766	14	US-10-156-239-17	Sequence 17, Appl
738	78.5	6.6	766	14	US-10-159-485-17	Sequence 17, Appl
739	78	6.5	355	9	US-09-938-719-9	Sequence 9, Appl1
740	78	6.5	355	9	US-09-939-703-9	Sequence 9, Appl1
741	78	6.5	355	16	US-10-661-798-9	Sequence 9, Appl1
742	78	6.5	355	16	US-10-612-791-9	Sequence 9, Appl1
743	78	6.5	355	16	US-10-612-791-9	Sequence 9, Appl1
744	78	6.5	411	9	US-09-815-442-11138	Sequence 11138, A
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746	77.5	6.5	280	15	US-10-243-552-905	Sequence 905, App
747	77.5	6.5	327	15	US-10-282-122A-76813	Sequence 76813, A
748	77.5	6.5	338	16	US-10-437-963-163107	Sequence 163107,
749	77.5	6.5	491	15	US-10-369-493-21395	Sequence 21395, A
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751	77.5	6.5	892	14	US-10-226-628A-15	Sequence 15, Appl
752	77	6.4	630	15	US-10-282-122A-44096	Sequence 44096, A
753	77	6.4	735	16	US-10-437-963-162148	Sequence 162148,

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755	76.5	6.4	453	13	US-10-437-963-156098	Sequence 156098,	828	73	6.1	377	9	US-09-939-980-533	Sequence 533, Appl
756	76.5	6.4	494	16	US-10-143-002-4	Sequence 4, Appl1	829	73	6.1	450	16	US-10-626-893-59	Sequence 59, Appl
757	76.5	6.4	555	14	US-10-325-891-4	Sequence 4, Appl1	830	73	6.1	453	15	US-10-282-182A-59343	Sequence 59343, A
758	76.5	6.4	555	15	US-10-104-047-2011	Sequence 2011, Ap	831	73	6.1	456	15	US-10-038-85A-30	Sequence 30, Appl
759	76.5	6.4	570	15	US-10-415-187-3	Sequence 3, Appl1	832	73	6.1	533	15	US-10-282-122A-59060	Sequence 59060, A
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761	76.5	6.4	593	15	US-10-335-977-6023	Sequence 6023, Ap	834	73	6.1	748	9	US-09-815-242-12792	Sequence 12792, A
762	76.5	6.4	638	15	US-10-424-599-214477	Sequence 214477,	835	73	6.1	750	10	US-09-746-788-86	Sequence 86, Appl
763	76.5	6.4	2539	15	US-10-369-493-3779	Sequence 3779, Ap	836	73	6.1	788	15	US-10-282-122A-70316	Sequence 70316, A
764	76	6.4	295	15	US-10-424-599-163113	Sequence 163113,	837	73	6.1	792	17	US-09-815-242-12327	Sequence 12327, A
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766	76	6.4	557	9	US-09-925-299-940	Sequence 940, App	839	73	6.1	806	16	US-10-437-963-173527	Sequence 173527,
767	76	6.4	557	10	US-09-925-299-940	Sequence 940, App	840	73	6.1	966	9	US-09-828-466-6	Sequence 6, Appl1
768	76	6.4	1402	15	US-10-369-493-5502	Sequence 5502, Ap	841	73	6.1	971	16	US-10-788-793-141	Sequence 141, App
769	76	6.4	1917	15	US-10-369-493-6036	Sequence 6036, Ap	842	73	6.1	971	17	US-10-624-727-49	Sequence 49, Appl
770	75.5	6.3	129	15	US-10-424-599-266695	Sequence 266695,	843	73	6.1	971	17	US-10-624-727-59	Sequence 59, Appl
771	75.5	6.3	233	16	US-10-437-963-188833	Sequence 188833,	844	72.5	6.1	209	14	US-10-080-170-107	Sequence 107, App
772	75.5	6.3	263	10	US-09-769-787-119	Sequence 119, App	845	72.5	6.1	209	16	US-10-080-170-107	Sequence 107, App
773	75.5	6.3	276	10	US-10-472-928-3518	Sequence 3518, Ap	846	72.5	6.1	209	16	US-10-468-356-107	Sequence 107, App
774	75.5	6.3	342	16	US-10-451-467A-528	Sequence 528, App	847	72.5	6.1	222	15	US-10-282-122A-43226	Sequence 43226, A
775	75.5	6.3	352	9	US-09-912-020-293	Sequence 293, App	848	72.5	6.1	222	15	US-10-424-599-205057	Sequence 205057,
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778	75	6.3	473	16	US-10-004-378A-104	Sequence 104, App	851	72.5	6.1	279	15	US-10-424-599-187241	Sequence 187241,
779	75	6.3	473	16	US-10-755-889-598	Sequence 598, App	852	72.5	6.1	233	15	US-10-424-599-163110	Sequence 163110,
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781	75	6.3	789	16	US-10-437-963-188379	Sequence 188379,	854	72.5	6.1	307	15	US-10-425-114-66808	Sequence 66808, A
782	75	6.3	874	16	US-10-437-963-153160	Sequence 153160,	855	72.5	6.1	307	15	US-10-425-114-67080	Sequence 67080, A
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784	74.5	6.2	263	16	US-10-437-963-149181	Sequence 149181,	857	72.5	6.1	310	15	US-10-425-114-66745	Sequence 66745, A
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786	74.5	6.2	355	9	US-09-789-486-4	Sequence 4, Appl1	859	72.5	6.1	311	15	US-10-425-114-65377	Sequence 65277, A
787	74.5	6.2	355	14	US-10-290-058A-3	Sequence 3, Appl1	860	72.5	6.1	312	15	US-10-425-114-66761	Sequence 66761, A
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789	74.5	6.2	355	14	US-10-225-567A-232	Sequence 232, App	862	72.5	6.1	389	15	US-10-350-924-1	Sequence 215, App
790	74.5	6.2	355	14	US-10-225-567A-249	Sequence 249, App	863	72.5	6.1	389	15	US-10-350-924-1	Sequence 1, Appl1
791	74.5	6.2	355	14	US-10-239-423-82	Sequence 82, App1	864	72.5	6.1	448	9	US-09-935-571-16	Sequence 16, Appl
792	74.5	6.2	355	16	US-10-741-601-367	Sequence 367, App	865	72.5	6.1	448	9	US-09-935-571-16	Sequence 16, Appl
793	74.5	6.2	355	16	US-10-741-600-1084	Sequence 1084, Ap	866	72.5	6.1	448	9	US-09-935-571-17	Sequence 17, Appl
794	74.5	6.2	362	16	US-10-741-601-368	Sequence 368, App	867	72.5	6.1	513	9	US-09-935-571-15	Sequence 15, Appl
795	74.5	6.2	362	17	US-10-741-600-1085	Sequence 1085, Ap	868	72.5	6.1	522	15	US-10-369-493-2418	Sequence 2418, Ap
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803	74	6.2	342	15	US-10-243-552-467	Sequence 467, App	876	72.5	6.1	1707	16	US-10-437-963-154005	Sequence 154005,
804	74	6.2	350	14	US-10-112-356-7	Sequence 7, Appl1	877	72	6.0	223	16	US-10-437-963-154005	Sequence 570, App
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818	73	6.1	114	15	US-10-335-977-8878	Sequence 8878, Ap	891	72	6.0	656	14	US-10-425-114-58050	Sequence 70316, A
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820	73	6.1	189	9	US-09-828-644-114	Sequence 114, App	893	72	6.0	656	14	US-10-241-220-83	Sequence 83, Appl
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823	73	6.1	272	14	US-10-156-911-75	Sequence 75, Appl	896	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl
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825	73	6.1	276	17	US-10-335-977-5928	Sequence 5928, Ap	898	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl
826	73	6.1	342	14	US-10-177-293-160	Sequence 160, App	899	72	6.0	741	14	US-10-270-786-11	Sequence 11, Appl

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902	72	6.0	2307	10	US-09-919-901-9	Sequence 9, Appl1	975	71	5.9	471	17	US-10-335-977-5539	Sequence 5539, Ap
903	72	6.0	2307	10	US-09-919-901-16	Sequence 16, Appl1	976	71	5.9	471	17	US-10-437-963-201663	Sequence 201663, Ap
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907	72	6.0	2307	14	US-10-191-966-16	Sequence 16, Appl1	980	71	5.9	471	17	US-10-437-963-119462	Sequence 119462, Ap
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910	71.5	6.0	363	16	US-10-768-878-8	Sequence 8, Appl1	983	71	5.9	471	17	US-10-335-977-5540	Sequence 5540, Ap
911	71.5	6.0	366	16	US-09-992-331-8	Sequence 8, Appl1	984	71	5.9	471	17	US-10-437-963-141086	Sequence 141086, Ap
912	71.5	6.0	382	9	US-09-971-228-5	Sequence 5, Appl1	985	71	5.9	471	17	US-10-437-963-131174	Sequence 131174, Ap
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914	71.5	6.0	382	10	US-09-759-514-2	Sequence 2, Appl1	987	70.5	5.9	471	17	US-10-767-701-60641	Sequence 60641, A
915	71.5	6.0	382	10	US-09-904-099-1	Sequence 1, Appl1	988	70.5	5.9	471	17	US-10-115-577A-64	Sequence 64, Appl1
916	71.5	6.0	382	13	US-10-087-192-786	Sequence 786, Ap	989	70.5	5.9	471	17	US-10-051-902-16	Sequence 16, Appl1
917	71.5	6.0	382	14	US-10-225-567A-237	Sequence 237, Ap	990	70.5	5.9	471	17	US-10-051-909-16	Sequence 16, Appl1
918	71.5	6.0	382	15	US-10-295-027-2	Sequence 2, Appl1	991	70.5	5.9	471	17	US-10-282-122A-45354	Sequence 45354, A
919	71.5	6.0	382	15	US-10-429-160-72	Sequence 72, Appl1	992	70.5	5.9	471	17	US-10-767-701-45405	Sequence 45405, A
920	71.5	6.0	382	15	US-10-211-462-2	Sequence 2, Appl1	993	70.5	5.9	471	17	US-10-425-114-62068	Sequence 62068, A
921	71.5	6.0	383	15	US-10-369-493-2267	Sequence 2267, Ap	994	70.5	5.9	471	17	US-10-437-963-191259	Sequence 191259, A
922	71.5	6.0	390	14	US-10-775-984-3	Sequence 3, Appl1	995	70.5	5.9	471	17	US-10-403-143-158	Sequence 158, Ap
923	71.5	6.0	394	14	US-10-394-136-51	Sequence 51, Appl1	996	70.5	5.9	471	17	US-10-262-313-9	Sequence 9, Appl1
924	71.5	6.0	405	15	US-10-424-599-149141	Sequence 149141, A	997	70.5	5.9	471	17	US-10-768-878-9	Sequence 9, Appl1
925	71.5	6.0	410	14	US-10-156-761-13608	Sequence 13608, A	998	70.5	5.9	471	17	US-10-060-902-32	Sequence 32, Appl1
926	71.5	6.0	433	16	US-10-437-963-156065	Sequence 156065, A	999	70.5	5.9	471	17	US-10-354-247-32	Sequence 32, Appl1
927	71.5	6.0	448	15	US-10-425-114-55760	Sequence 55760, A	1000	70.5	5.9	471	17	US-09-992-331-9	Sequence 9, Appl1
928	71.5	6.0	524	15	US-10-282-122A-53957	Sequence 53957, A	1001	70.5	5.9	471	17	US-10-369-493-10462	Sequence 10462, A
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931	71.5	6.0	568	9	US-09-843-856-2	Sequence 2, Appl1	1004	70.5	5.9	471	17	US-10-060-902-16	Sequence 16, Appl1
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934	71.5	6.0	697	10	US-09-371-347-46	Sequence 46, Appl1	1007	70.5	5.9	471	17	US-10-060-902-24	Sequence 24, Appl1
935	71.5	6.0	698	10	US-09-371-347-2	Sequence 2, Appl1	1008	70.5	5.9	471	17	US-10-354-247-22	Sequence 22, Appl1
936	71.5	6.0	698	10	US-09-371-347-21	Sequence 21, Appl1	1009	70.5	5.9	471	17	US-10-354-247-24	Sequence 24, Appl1
937	71.5	6.0	698	10	US-09-371-347-42	Sequence 42, Appl1	1010	70.5	5.9	471	17	US-10-060-902-28	Sequence 28, Appl1
938	71.5	6.0	698	10	US-09-371-347-44	Sequence 44, Appl1	1011	70.5	5.9	471	17	US-10-060-902-36	Sequence 36, Appl1
939	71.5	6.0	698	17	US-10-741-600-1520	Sequence 1520, Ap	1012	70.5	5.9	471	17	US-10-354-247-28	Sequence 28, Appl1
940	71.5	6.0	725	13	US-10-741-600-1521	Sequence 1521, Ap	1013	70.5	5.9	471	17	US-10-354-247-36	Sequence 36, Appl1
941	71.5	6.0	890	17	US-10-060-425-2	Sequence 2, Appl1	1014	70.5	5.9	471	17	US-10-225-567A-294	Sequence 294, Ap
942	71.5	6.0	2560	15	US-10-276-774-1774	Sequence 1774, Ap	1015	70.5	5.9	471	17	US-10-060-902-34	Sequence 34, Appl1
943	71.5	6.0	2923	9	US-09-788-711A-4	Sequence 4, Appl1	1016	70.5	5.9	471	17	US-10-354-247-34	Sequence 34, Appl1
944	71.5	6.0	2923	10	US-09-916-849A-3	Sequence 3, Appl1	1017	70.5	5.9	471	17	US-10-060-902-18	Sequence 18, Appl1
945	71.5	6.0	2923	14	US-10-225-567A-554	Sequence 524, Ap	1018	70.5	5.9	471	17	US-10-354-247-18	Sequence 18, Appl1
946	71.5	6.0	2923	14	US-10-174-677-29	Sequence 29, Appl1	1019	70.5	5.9	471	17	US-10-060-902-26	Sequence 26, Appl1
947	71.5	6.0	2923	15	US-10-120-801-53	Sequence 53, Appl1	1020	70.5	5.9	471	17	US-10-354-247-26	Sequence 26, Appl1
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949	71.5	6.0	2923	15	US-10-038-854-70	Sequence 70, Appl1	1022	70.5	5.9	471	17	US-10-354-247-20	Sequence 20, Appl1
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956	71	5.9	438	16	US-10-437-963-181098	Sequence 181098, A	1029	70.5	5.9	471	17	US-10-369-493-5442	Sequence 5442, Ap
957	71	5.9	444	15	US-10-287-226-370	Sequence 370, Ap	1030	70.5	5.9	471	17	US-09-845-908-11	Sequence 11, Appl1
958	71	5.9	444	15	US-10-287-226-372	Sequence 372, Ap	1031	70.5	5.9	471	17	US-09-925-300-1299	Sequence 1299, Ap
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966	71	5.9	471	14	US-10-251-385-122	Sequence 122, Ap	1039	70.5	5.9	471	17	US-10-428-487-16	Sequence 16, Appl1
967	71	5.9	471	14	US-10-251-385-228	Sequence 228, Ap	1040	70.5	5.9	471	17	US-10-211-465-44	Sequence 44, Appl1
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970	71	5.9	471	14	US-10-092-138-28	Sequence 28, Appl1	1043	70	5.9	471	17	US-09-908-008A-41	Sequence 41, Appl1
971	71	5.9	471	17	US-10-741-600-1461	Sequence 1461, Ap	1044	70	5.9	471	17	US-09-908-008A-44	Sequence 44, Appl1
972	71	5.9	471	17	US-10-741-600-1462	Sequence 1462, Ap	1045	70	5.9	471	17	US-10-251-385-16	Sequence 16, Appl1

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1047	70	5.9	333	14	US-10-225-567A-279	Sequence 279, App	1120	69	5.8	388	9	US-09-912-020-378	Sequence 378, App
1048	70	5.9	333	15	US-10-433-561-32	Sequence 32, App	1121	69	5.8	388	15	US-10-282-122A-42742	Sequence 42742, A
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1059	70	5.9	475	15	US-10-297-022-24	Sequence 24, App1	1132	69	5.8	1133	16	US-10-437-963-189159	Sequence 189159, A
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1062	70	5.9	637	15	US-10-282-122A-61377	Sequence 61377, A	1135	69	5.8	112	14	US-10-115-571A-40	Sequence 40, App1
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1083	69.5	5.8	490	15	US-10-369-493-17545	Sequence 17545, A	1156	68.5	5.7	444	9	US-09-191-724-11	Sequence 11, App1
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1085	69.5	5.8	540	15	US-10-354-437-54	Sequence 54, App1	1158	68.5	5.7	444	15	US-10-649-199-15	Sequence 15, App1
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1090	69.5	5.8	557	17	US-10-327-188-4	Sequence 4, App1	1163	68.5	5.7	468	17	US-10-925-095-553	Sequence 553, App
1091	69.5	5.8	557	17	US-10-940-500-1	Sequence 1, App1	1164	68.5	5.7	475	9	US-09-935-371-26	Sequence 26, App1
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1101	69.5	5.8	877	15	US-10-369-493-22547	Sequence 22547, A	1174	68.5	5.7	525	15	US-10-295-027-276	Sequence 276, App
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1103	69.5	5.8	1704	14	US-10-340-097-120	Sequence 120, App	1176	68.5	5.7	548	10	US-09-809-391-469	Sequence 469, App
1104	69.5	5.8	1704	14	US-10-336-219-120	Sequence 120, App	1177	68.5	5.7	548	10	US-09-882-171-469	Sequence 469, App
1105	69.5	5.8	1704	14	US-10-336-219-120	Sequence 120, App	1178	68.5	5.7	548	15	US-10-164-861-469	Sequence 469, App
1106	69.5	5.8	1704	14	US-10-408-765A-22220	Sequence 2220, App	1179	68.5	5.7	548	15	US-10-440-464-88	Sequence 88, App1
1107	69.5	5.8	1704	16	US-10-648-593-213	Sequence 213, App	1180	68.5	5.7	552	9	US-09-935-371-27	Sequence 27, App1
1108	69	5.8	214	9	US-09-844-864-17	Sequence 17, App1	1181	68.5	5.7	553	9	US-09-935-371-25	Sequence 25, App1
1109	69	5.8	214	15	US-10-108-260A-2534	Sequence 2534, App	1182	68.5	5.7	553	15	US-10-424-599-253232	Sequence 253232, A
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1111	69	5.8	321	17	US-10-774-355A-2034	Sequence 2034, App	1184	68.5	5.7	588	17	US-10-741-844-7067	Sequence 7067, App
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1117	69	5.8	370	14	US-10-278-087A-26	Sequence 26, App1	1190	68.5	5.7	1004	15	US-10-369-493-1668	Sequence 1668, App
1118	69	5.8	380	16	US-10-611-210-11	Sequence 11, App1	1191	68.5	5.7				

1192	68.5	5.7	1178	15	US-10-320-797-3347	Sequence 3347, Ap	1265	68	5.7	471	10	US-09-951-217-28	Sequence 28, Appl
1193	68.5	5.7	1211	14	US-10-017-161-824	Sequence 824, App	1266	68	5.7	471	14	US-10-032-588-7028	Sequence 7028, Ap
1194	68.5	5.7	1236	16	US-10-208-731-9	Sequence 9, Appl1	1267	68	5.7	471	17	US-10-882-104-88	Sequence 88, Appl
1195	68.5	5.7	1378	16	US-10-437-963-157709	Sequence 157709,	1268	68	5.7	472	10	US-09-951-217-36	Sequence 36, Appl
1196	68	5.7	143	16	US-10-767-701-36814	Sequence 36814, A	1269	68	5.7	482	15	US-10-424-599-249130	Sequence 249130,
1197	68	5.7	247	9	US-09-738-626-5109	Sequence 5109, Ap	1270	68	5.7	488	10	US-09-826-509-561	Sequence 561, App
1198	68	5.7	258	14	US-10-023-171-7	Sequence 7, Appl1	1271	68	5.7	488	14	US-10-225-556A-296	Sequence 296, App
1199	68	5.7	273	14	US-10-183-116-85	Sequence 85, Appl	1272	68	5.7	488	14	US-10-320-351-3	Sequence 3, Appl1
1200	68	5.7	273	14	US-10-357-135-85	Sequence 85, Appl	1273	68	5.7	488	15	US-10-295-022-1326	Sequence 1326, Ap
1201	68	5.7	279	15	US-10-174-364-58	Sequence 58, Appl	1274	68	5.7	488	16	US-10-735-888-1170	Sequence 170, App
1202	68	5.7	295	15	US-10-246-583-58	Sequence 58, Appl	1275	68	5.7	488	17	US-10-925-099-561	Sequence 561, App
1203	68	5.7	295	15	US-10-108-260A-4304	Sequence 4304, Ap	1276	68	5.7	488	17	US-10-688-790-18	Sequence 18, Appl
1204	68	5.7	313	15	US-10-424-599-239229	Sequence 239229,	1277	68	5.7	490	14	US-10-243-501-3	Sequence 3, Appl1
1205	68	5.7	324	16	US-10-767-701-45081	Sequence 45081, A	1278	68	5.7	490	14	US-10-243-351-2	Sequence 2, Appl1
1206	68	5.7	326	17	US-10-688-790-4	Sequence 4, Appl1	1279	68	5.7	519	16	US-10-437-963-14353	Sequence 12453,
1207	68	5.7	326	17	US-10-688-790-6	Sequence 6, Appl1	1280	68	5.7	519	16	US-10-369-493-913	Sequence 913, App
1208	68	5.7	330	9	US-09-826-791-2	Sequence 2, Appl1	1281	68	5.7	519	16	US-10-369-493-913	Sequence 913, App
1209	68	5.7	330	9	US-09-991-225-2	Sequence 2, Appl1	1282	68	5.7	519	16	US-10-282-122A-65907	Sequence 65907, A
1210	68	5.7	330	15	US-10-369-405-2	Sequence 2, Appl1	1283	68	5.7	519	16	US-10-275-026A-8	Sequence 8, Appl1
1211	68	5.7	341	10	US-09-991-225-55	Sequence 55, Appl	1284	68	5.7	519	16	US-10-275-026A-76	Sequence 76, Appl
1212	68	5.7	341	10	US-10-369-405-55	Sequence 55, Appl	1285	68	5.7	519	16	US-10-275-026A-92	Sequence 92, Appl
1213	68	5.7	346	9	US-09-826-791-6	Sequence 6, Appl1	1286	68	5.7	519	16	US-10-369-493-4101	Sequence 4101, Ap
1214	68	5.7	346	9	US-09-866-230-7	Sequence 7, Appl1	1287	68	5.7	519	16	US-10-090-453-13	Sequence 13, Appl
1215	68	5.7	346	9	US-09-866-230-9	Sequence 9, Appl1	1288	68	5.7	519	16	US-10-437-963-195183	Sequence 195183,
1216	68	5.7	346	9	US-09-828-478-2	Sequence 2, Appl1	1289	68	5.7	519	16	US-09-923-444A-2	Sequence 2, Appl1
1217	68	5.7	346	10	US-09-779-679-2	Sequence 2, Appl1	1290	68	5.7	519	16	US-10-276-774-2313	Sequence 2313, Ap
1218	68	5.7	346	10	US-09-779-679-26	Sequence 26, Appl	1291	68	5.7	519	16	US-10-213-439-2	Sequence 2, Appl1
1219	68	5.7	346	10	US-09-991-225-30	Sequence 30, Appl	1292	68	5.7	519	16	US-10-213-439-2	Sequence 2, Appl1
1220	68	5.7	346	11	US-09-980-049-1	Sequence 1, Appl1	1293	68	5.7	519	16	US-10-213-439-4	Sequence 4, Appl1
1221	68	5.7	346	14	US-10-225-567A-589	Sequence 589, App	1294	68	5.7	519	16	US-10-788-266-4	Sequence 4, Appl1
1222	68	5.7	346	14	US-10-349-021-2	Sequence 2, Appl1	1295	68	5.7	519	16	US-09-753-008-7	Sequence 7, Appl1
1223	68	5.7	346	14	US-10-321-807-14	Sequence 14, Appl	1296	68	5.7	519	16	US-10-437-963-166382	Sequence 166382,
1224	68	5.7	346	14	US-10-321-807-88	Sequence 88, Appl	1297	68	5.7	519	16	US-10-767-701-34938	Sequence 34938, A
1225	68	5.7	346	15	US-10-131-332A-2	Sequence 2, Appl1	1298	68	5.7	519	16	US-10-115-571A-6	Sequence 54, Appl
1226	68	5.7	346	15	US-10-369-405-30	Sequence 30, Appl	1299	68	5.7	519	16	US-10-437-963-179142	Sequence 179142,
1227	68	5.7	346	15	US-10-182-605-2	Sequence 2, Appl1	1300	68	5.7	519	16	US-10-425-11-39064	Sequence 39064, A
1228	68	5.7	346	15	US-10-403-161-22	Sequence 22, Appl	1301	68	5.7	519	16	US-10-437-963-104940	Sequence 104940,
1229	68	5.7	346	15	US-10-403-161-24	Sequence 24, Appl	1302	68	5.7	519	16	US-10-032-588-7603	Sequence 7603, Ap
1230	68	5.7	346	15	US-10-343-650A-58	Sequence 58, Appl	1303	68	5.7	519	16	US-10-437-963-188884	Sequence 188884,
1231	68	5.7	346	15	US-10-297-247-2	Sequence 2, Appl1	1304	68	5.7	519	16	US-10-437-963-159513	Sequence 159513,
1232	68	5.7	346	16	US-10-321-807-14	Sequence 14, Appl	1305	68	5.7	519	16	US-10-774-355A-2077	Sequence 2077, Ap
1233	68	5.7	346	16	US-10-321-807-88	Sequence 88, Appl	1306	68	5.7	519	16	US-10-282-122A-67484	Sequence 67484, A
1234	68	5.7	346	16	US-10-314-048A-14	Sequence 14, Appl	1307	68	5.7	519	16	US-10-932-004-18	Sequence 18, Appl
1235	68	5.7	346	16	US-10-314-048A-88	Sequence 88, Appl	1308	68	5.7	519	16	US-10-403-161-12	Sequence 12, Appl
1236	68	5.7	346	16	US-10-157-262-40	Sequence 40, Appl	1309	68	5.7	519	16	US-09-765-994-4	Sequence 4, Appl1
1237	68	5.7	346	16	US-10-897-815-14	Sequence 14, Appl	1310	68	5.7	519	16	US-09-765-994-2	Sequence 2, Appl1
1238	68	5.7	346	16	US-10-897-815-88	Sequence 88, Appl	1311	68	5.7	519	16	US-09-765-994-8	Sequence 8, Appl1
1239	68	5.7	346	17	US-10-932-004-2	Sequence 2, Appl1	1312	68	5.7	519	16	US-09-968-433-16	Sequence 16, Appl
1240	68	5.7	346	17	US-10-435-828-2	Sequence 2, Appl1	1313	68	5.7	519	16	US-10-282-837-8	Sequence 8, Appl1
1241	68	5.7	350	17	US-10-688-790-2	Sequence 2, Appl1	1314	68	5.7	519	16	US-10-225-567A-607	Sequence 607, App
1242	68	5.7	355	9	US-09-961-068-1	Sequence 1, Appl1	1315	68	5.7	519	16	US-10-288-222A-10	Sequence 10, Appl
1243	68	5.7	355	9	US-09-960-547-1	Sequence 1, Appl1	1316	68	5.7	519	16	US-10-145-588-8	Sequence 8, Appl1
1244	68	5.7	355	9	US-09-886-319A-14	Sequence 14, Appl	1317	68	5.7	519	16	US-10-239-423-75	Sequence 75, Appl
1245	68	5.7	355	14	US-09-893-512-11	Sequence 11, Appl	1318	68	5.7	519	16	US-10-407-079-84	Sequence 84, Appl
1246	68	5.7	355	14	US-10-039-659-13	Sequence 13, Appl	1319	68	5.7	519	16	US-10-698-959-2	Sequence 2, Appl1
1247	68	5.7	355	14	US-10-225-567A-62	Sequence 62, Appl	1320	68	5.7	519	16	US-10-403-571-100	Sequence 100, App
1248	68	5.7	355	14	US-10-245-850-2	Sequence 2, Appl1	1321	68	5.7	519	16	US-09-944-045-2	Sequence 2, Appl1
1249	68	5.7	355	14	US-10-376-564-14	Sequence 14, Appl	1322	68	5.7	519	16	US-09-944-045-4	Sequence 4, Appl1
1250	68	5.7	355	14	US-10-339-423-62	Sequence 62, Appl	1323	68	5.7	519	16	US-09-944-045-48	Sequence 48, Appl
1251	68	5.7	355	14	US-10-439-845-9	Sequence 9, Appl1	1324	68	5.7	519	16	US-10-182-960-13	Sequence 10, Appl
1252	68	5.7	355	14	US-10-452-015-2	Sequence 2, Appl1	1325	68	5.7	519	16	US-10-282-122A-49613	Sequence 49613, A
1253	68	5.7	355	16	US-10-754-071-13	Sequence 13, Appl	1326	68	5.7	519	16	US-10-282-122A-60581	Sequence 60581, A
1254	68	5.7	355	16	US-10-755-889-582	Sequence 582, App	1327	68	5.7	519	16	US-09-741-669-385	Sequence 385, App
1255	68	5.7	355	17	US-10-759-860-13	Sequence 13, Appl	1328	68	5.7	519	16	US-10-282-122A-70288	Sequence 70288, A
1256	68	5.7	357	15	US-10-282-122A-72564	Sequence 72564, A	1329	68	5.7	519	16	US-10-831-399-3	Sequence 3, Appl1
1257	68	5.7	375	14	US-10-219-834-78	Sequence 78, Appl	1330	68	5.7	519	16	US-10-831-399-8	Sequence 8, Appl1
1258	68	5.7	393	15	US-10-382-122A-78245	Sequence 78245, A	1331	68	5.7	519	16	US-10-369-493-1060	Sequence 1060, Ap
1259	68	5.7	393	15	US-10-282-122A-59444	Sequence 59444, A	1332	68	5.7	519	16	US-09-892-851-2	Sequence 2, Appl1
1260	68	5.7	396	15	US-10-282-122A-50261	Sequence 50261, A	1333	68	5.7	519	16	US-10-897-019-2	Sequence 2, Appl1
1261	68	5.7	423	14	US-10-425-114-45853	Sequence 45853, A	1334	68	5.7	519	16	US-10-289-766-369	Sequence 369, App
1262	68	5.7	426	15	US-10-328-459-2	Sequence 2, Appl1	1335	68	5.7	519	16	US-10-424-599-179430	Sequence 179430,
1263	68	5.7	469	15	US-10-369-493-13470	Sequence 13470, A	1336	68	5.7	519	16	US-10-177-299-476	Sequence 476, App
1264	68	5.7	471	10	US-09-951-217-8	Sequence 8, Appl1	1337	68	5.7	519	16	US-10-437-963-114005	Sequence 114005,

1338	67.5	5.6	608	15	US-10-108-260A-4385	Sequence 4385, Ap	1411	67	5.6	978	14	US-10-270-855-20	Sequence 20, Appl
1339	67.5	5.6	632	10	US-09-820-843A-25	Sequence 25, Appl	1412	67	5.6	978	14	US-10-270-846-20	Sequence 20, Appl
1340	67.5	5.6	673	15	US-10-403-571-146	Sequence 146, App	1413	67	5.6	1233	17	US-10-741-879-7139	Sequence 7139, Ap
1341	67.5	5.6	681	15	US-10-451-822-26	Sequence 26, Appl	1414	67	5.6	1242	9	US-09-904-065-12	Sequence 12, Appl
1342	67.5	5.6	744	15	US-10-282-122A-50942	Sequence 50942, A	1415	67	5.6	1242	9	US-09-904-065-13	Sequence 12, Appl
1343	67.5	5.6	751	16	US-10-437-963-165566	Sequence 165566, Sequence 2, Appl1	1416	67	5.6	1242	16	US-10-692-556-12	Sequence 12, Appl
1344	67.5	5.6	797	14	US-10-214-390-2	Sequence 2, Appl1	1417	67	5.6	1242	16	US-10-692-556-13	Sequence 12, Appl
1345	67.5	5.6	805	15	US-10-429-160-60	Sequence 60, Appl1	1418	67	5.6	1511	15	US-09-801-368-250	Sequence 250, Appl
1346	67.5	5.6	832	16	US-10-437-963-161692	Sequence 161692, Sequence 22174, A	1419	67	5.6	1511	15	US-10-310-154-393	Sequence 393, App
1347	67.5	5.6	888	15	US-10-369-493-122114	Sequence 122114, A	1420	67	5.6	1511	15	US-10-369-493-22280	Sequence 2280, A
1348	67.5	5.6	921	16	US-10-467-685-14	Sequence 14, Appl1	1421	67	5.6	3010	15	US-10-467-000-1	Sequence 1, Appl1
1349	67.5	5.6	927	16	US-10-408-765A-2938	Sequence 2938, Ap	1422	66.5	5.6	108	15	US-10-424-599-182659	Sequence 182659, Sequence 53694, A
1350	67.5	5.6	1147	16	US-10-437-963-110474	Sequence 110474, Sequence 2418, Ap	1423	66.5	5.6	195	15	US-10-425-114-53694	Sequence 53694, A
1351	67.5	5.6	1313	9	US-10-408-765A-2418	Sequence 2418, Ap	1424	66.5	5.6	204	14	US-10-080-170-561	Sequence 561, App
1352	67.5	5.6	1324	16	US-09-935-371-56	Sequence 3723, Ap	1425	66.5	5.6	204	16	US-10-468-356-561	Sequence 561, App
1353	67.5	5.6	1652	15	US-10-369-493-3223	Sequence 3223, Ap	1426	66.5	5.6	253	15	US-10-094-744-2531	Sequence 2531, Ap
1354	67.5	5.6	1907	15	US-10-437-963-157069	Sequence 157069, Sequence 157067, Sequence 222, App	1427	66.5	5.6	272	15	US-10-425-114-72322	Sequence 72322, A
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1356	67.5	5.6	2158	15	US-10-341-434-222	Sequence 34, Appl1	1429	66.5	5.6	272	15	US-10-424-599-254464	Sequence 254464, Sequence 431, App
1357	67.5	5.6	2158	15	US-10-144-198-34	Sequence 35, Appl1	1430	66.5	5.6	304	14	US-09-804-291-431	Sequence 394, App
1358	67.5	5.6	2265	16	US-10-408-765A-624	Sequence 624, App	1431	66.5	5.6	304	10	US-10-017-161-394	Sequence 394, App
1359	67.5	5.6	2265	16	US-10-144-198-35	Sequence 12, Appl1	1432	66.5	5.6	304	14	US-10-017-161-394	Sequence 554, App
1360	67.5	5.6	2697	15	US-10-144-198-12	Sequence 71, Appl1	1433	66.5	5.6	304	14	US-10-025-806-60	Sequence 60, Appl1
1361	67.5	5.6	2920	15	US-10-038-854-71	Sequence 2, Appl1	1434	66.5	5.6	304	14	US-10-025-806-62	Sequence 62, Appl1
1362	67.5	5.6	3542	15	US-10-087-013-2	Sequence 57539, A	1435	66.5	5.6	304	15	US-10-292-798-352	Sequence 352, App
1363	67	5.6	136	16	US-10-767-701-57539	Sequence 329, App	1436	66.5	5.6	304	15	US-10-343-650A-632	Sequence 632, App
1364	67	5.6	153	15	US-10-289-762-329	Sequence 1312, Ap	1437	66.5	5.6	304	16	US-10-467-252-42	Sequence 42, Appl1
1365	67	5.6	184	14	US-10-017-161-1312	Sequence 1078, Ap	1438	66.5	5.6	308	15	US-10-424-599-195171	Sequence 195171, Sequence 1690, Ap
1366	67	5.6	184	14	US-10-292-798-1078	Sequence 63844, A	1439	66.5	5.6	316	17	US-10-774-355A-1690	Sequence 1690, Ap
1367	67	5.6	185	15	US-10-425-114-63844	Sequence 32, Appl1	1440	66.5	5.6	345	13	US-10-051-902-14	Sequence 14, Appl1
1368	67	5.6	199	13	US-10-104-019-32	Sequence 32, Appl1	1441	66.5	5.6	345	13	US-10-051-902-14	Sequence 14, Appl1
1369	67	5.6	199	14	US-10-104-019-32	Sequence 32, Appl1	1442	66.5	5.6	345	13	US-10-051-902-14	Sequence 14, Appl1
1370	67	5.6	200	14	US-10-428-826-32	Sequence 22568, A	1443	66.5	5.6	347	15	US-10-262-511-154	Sequence 154, App
1371	67	5.6	292	15	US-10-369-493-22568	Sequence 7472, Ap	1444	66.5	5.6	359	9	US-09-828-523A-14	Sequence 14, Appl1
1372	67	5.6	304	14	US-10-032-585-7472	Sequence 75550, A	1445	66.5	5.6	359	14	US-09-966-591-12	Sequence 12, Appl1
1373	67	5.6	309	15	US-10-282-122A-57550	Sequence 1501, Ap	1446	66.5	5.6	370	9	US-09-828-523A-74	Sequence 74, Appl1
1374	67	5.6	334	16	US-10-408-765A-1501	Sequence 12590, A	1447	66.5	5.6	370	9	US-09-966-591-78	Sequence 78, Appl1
1375	67	5.6	335	14	US-10-156-761-12590	Sequence 51810, A	1448	66.5	5.6	370	14	US-10-429-094-78	Sequence 78, Appl1
1376	67	5.6	336	15	US-10-282-122A-51810	Sequence 11783, Sequence 1390, Ap	1449	66.5	5.6	384	14	US-10-363-678-3	Sequence 3, Appl1
1377	67	5.6	422	16	US-10-437-963-117783	Sequence 11783, Sequence 110, App	1450	66.5	5.6	384	15	US-10-373-801-32	Sequence 32, Appl1
1378	67	5.6	423	17	US-10-472-928-1390	Sequence 110, App	1451	66.5	5.6	384	15	US-10-472-928-406	Sequence 406, App
1379	67	5.6	449	17	US-09-769-787-110	Sequence 65537, A	1452	66.5	5.6	392	15	US-10-282-122A-56849	Sequence 56849, A
1380	67	5.6	485	15	US-10-425-114-65537	Sequence 247, App	1453	66.5	5.6	397	15	US-10-425-114-59163	Sequence 59163, A
1381	67	5.6	496	15	US-10-170-385-247	Sequence 89, Appl1	1454	66.5	5.6	399	16	US-10-767-701-46276	Sequence 46276, A
1382	67	5.6	496	16	US-10-341-434-89	Sequence 666, App	1455	66.5	5.6	409	13	US-10-157-855-22	Sequence 225, Appl1
1383	67	5.6	496	16	US-10-755-889-666	Sequence 39224, A	1456	66.5	5.6	413	16	US-10-474-776-235	Sequence 235, Appl1
1384	67	5.6	499	15	US-10-425-114-39224	Sequence 41, Appl1	1457	66.5	5.6	413	17	US-10-474-776-235	Sequence 544, App
1385	67	5.6	506	17	US-10-818-939-41	Sequence 52026, Sequence 3702, Ap	1458	66.5	5.6	435	16	US-10-472-928-544	Sequence 403, App
1386	67	5.6	507	15	US-10-403-571-52	Sequence 8, Appl1	1459	66.5	5.6	435	17	US-10-472-928-406	Sequence 4406, App
1387	67	5.6	523	15	US-10-424-599-220226	Sequence 3702, Ap	1460	66.5	5.6	437	16	US-10-437-963-193793	Sequence 2330, Ap
1388	67	5.6	586	15	US-10-369-493-3702	Sequence 8, Appl1	1461	66.5	5.6	477	15	US-10-335-977-6100	Sequence 6100, Ap
1389	67	5.6	627	14	US-10-090-455-8	Sequence 310, App	1462	66.5	5.6	477	15	US-10-335-977-6100	Sequence 6100, Ap
1390	67	5.6	627	15	US-10-267-502-310	Sequence 9, Appl1	1463	66.5	5.6	478	16	US-10-437-963-189400	Sequence 189400, Sequence 5640, Ap
1391	67	5.6	646	13	US-10-072-621-9	Sequence 4, Appl1	1464	66.5	5.6	480	15	US-10-335-977-5640	Sequence 5640, Ap
1392	67	5.6	646	13	US-10-154-452-4	Sequence 8, Appl1	1465	66.5	5.6	480	15	US-10-369-493-16555	Sequence 16555, A
1393	67	5.6	646	13	US-10-154-452-8	Sequence 2, Appl1	1466	66.5	5.6	480	15	US-10-369-493-16555	Sequence 16555, A
1394	67	5.6	646	14	US-10-090-455-2	Sequence 308, App	1467	66.5	5.6	495	14	US-10-156-761-10814	Sequence 10814, A
1395	67	5.6	646	14	US-10-332-447-3	Sequence 308, App	1468	66.5	5.6	504	16	US-10-437-963-169377	Sequence 169377, Sequence 169377, A
1396	67	5.6	646	15	US-10-267-502-308	Sequence 2399, Ap	1469	66.5	5.6	531	15	US-10-369-493-12512	Sequence 12512, A
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1402	67	5.6	884	15	US-10-346-000A-9	Sequence 9, Appl1	1475	66.5	5.6	614	14	US-10-145-012-13	Sequence 13, Appl1
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